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NEWS 1		Web Page URLs for STN Seminar Schedule - N. America
NEWS 2	Apr 08	"Ask CAS" for self-help around the clock
NEWS 3	Jun 03	New e-mail delivery for search results now available
NEWS 4	Aug 08	PHARMAMarketLetter(PHARMAML) - new on STN
NEWS 5	Aug 19	Aquatic Toxicity Information Retrieval (AQUIRE) now available on STN
NEWS 6	Aug 26	Sequence searching in REGISTRY enhanced
NEWS 7	Sep 03	JAPIO has been reloaded and enhanced
NEWS 8	Sep 16	Experimental properties added to the REGISTRY file
NEWS 9	Sep 16	CA Section Thesaurus available in CAPLUS and CA
NEWS 10	Oct 01	CASREACT Enriched with Reactions from 1907 to 1985
NEWS 11	Oct 24	BEILSTEIN adds new search fields
NEWS 12	Oct 24	Nutraceuticals International (NUTRACEUT) now available on STN
NEWS 13	Nov 18	DKILIT has been renamed APOLLIT
NEWS 14	Nov 25	More calculated properties added to REGISTRY
NEWS 15	Dec 04	CSA files on STN
NEWS 16	Dec 17	PCTFULL now covers WP/PCT Applications from 1978 to date
NEWS 17	Dec 17	TOXCENTER enhanced with additional content
NEWS 18	Dec 17	Adis Clinical Trials Insight now available on STN
NEWS 19	Jan 29	Simultaneous left and right truncation added to COMPENDEX, ENERGY, INSPEC
NEWS 20	Feb 13	CANCERLIT is no longer being updated
NEWS 21	Feb 24	METADEX enhancements
NEWS 22	Feb 24	PCTGEN now available on STN
NEWS 23	Feb 24	TEMA now available on STN
NEWS 24	Feb 26	NTIS now allows simultaneous left and right truncation
NEWS 25	Feb 26	PCTFULL now contains images
NEWS 26	Mar 04	SDI PACKAGE for monthly delivery of multifile SDI results
NEWS 27	Mar 20	EVENTLINE will be removed from STN
NEWS 28	Mar 24	PATDPAFULL now available on STN
NEWS 29	Mar 24	Additional information for trade-named substances without structures available in REGISTRY
NEWS 30	Apr 11	Display formats in DGENE enhanced
NEWS 31	Apr 14	MEDLINE Reload
NEWS 32	Apr 17	Polymer searching in REGISTRY enhanced
NEWS 33	Apr 21	Indexing from 1947 to 1956 being added to records in CA/CAPLUS
NEWS 34	Apr 21	New current-awareness alert (SDI) frequency in WPIDS/WPINDEX/WPIX
NEWS 35	Apr 28	RDISCLOSURE now available on STN
NEWS 36	May 05	Pharmacokinetic information and systematic chemical names added to PHAR
NEWS 37	May 15	MEDLINE file segment of TOXCENTER reloaded
NEWS 38	May 15	Supporter information for ENCOMPPAT and ENCOMPLIT updated
NEWS 39	May 16	CHEMREACT will be removed from STN
NEWS 40	May 19	Simultaneous left and right truncation added to WSCA
NEWS 41	May 19	RAPRA enhanced with new search field, simultaneous left and

right truncation

NEWS EXPRESS April 4 CURRENT WINDOWS VERSION IS V6.01a, CURRENT
MACINTOSH VERSION IS V6.0b(ENG) AND V6.0Jb(JP),
AND CURRENT DISCOVER FILE IS DATED 01 APRIL 2003
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FILE 'HOME' ENTERED AT 13:02:29 ON 26 MAY 2003

=> FIL MEDLINE BIOSIS EMBASE CA SCISEARCH
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FULL ESTIMATED COST 0.21 0.21

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FILE 'BIOSIS' ENTERED AT 13:02:49 ON 26 MAY 2003
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=> s antisense or (comple (2n) (oligo? or nuclei?))
L1 101549 ANTISENSE OR (COMPLE (2N) (OLIGO? OR NUCLEI?))

=> s antisense? or (comple? (2n) (oligo? or nuclei?))
<------User Break------>

SEARCH ENDED BY USER

=> s antisense? or (comple? (2n) (oligo? or nucle?))
4 FILES SEARCHED...
L2 217407 ANTISENSE? OR (COMPLE? (2N) (OLIGO? OR NUCLE?))

=> s ssdna or (singl? strand? (2n) (dna or rna or (nucle? acid?))
UNMATCHED LEFT PARENTHESIS 'OR (SINGL?'
The number of right parentheses in a query must be equal to the number of left parentheses.

```
=> s ssdna or (singl? strand? (2n) (dna or rna or (nucle? acid?)))
   3 FILES SEARCHED...
L3       77824 SSDNA OR (SINGL? STRAND? (2N) (DNA OR RNA OR (NUCLE? ACID?)))

=> s l2 and l3
L4        4019 L2 AND L3

=> s l2 (5n) l3
L5         603 L2 (5N) L3

=> s l2 (3n) l3
L6         474 L2 (3N) L3

=> s l6 and m13
L7          26 L6 AND M13

=> dup rem l7
PROCESSING COMPLETED FOR L7
L8           15 DUP REM L7 (11 DUPLICATES REMOVED)

=> d l8 1-15 ibib abs

L8   ANSWER 1 OF 15  CA  COPYRIGHT 2003 ACS
ACCESSION NUMBER:        137:380940  CA
TITLE:                   Unigene unidirectional antisense library derived from
                         recombinant bacteriophage or phagemid vector for
                         therapy and massive functional genomics
INVENTOR(S):             Park, Jong-Gu; Moon, Ik-Jae; Lee, Yun-Han
PATENT ASSIGNEE(S):      Welgene Pharmaceuticals, Inc., S. Korea
SOURCE:                  PCT Int. Appl., 79 pp.
                         CODEN: PIXXD2
DOCUMENT TYPE:           Patent
LANGUAGE:                English
FAMILY ACC. NUM. COUNT:  2
PATENT INFORMATION:

     PATENT NO.        KIND  DATE           APPLICATION NO.   DATE
     ---------------   ----  --------       ---------------   --------
     WO 2002092807      A1   20021121       WO 2002-IB1753    20020516
         W:  AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN,
             CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH,
             GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR,
             LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH,
             PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ,
             UA, UG, US, UZ, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU,
             TJ, TM
         RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, CH,
             CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR,
             BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG
PRIORITY APPLN. INFO.:                  KR 2001-27071    A  20010517
AB   The present invention provides a high throughput system for functional
     genomics using a unigene antisense library comprising large circular
     (LC)-antisense compds.  The said large circular (LC)-antisense compds are
     derived from recombinant bacteriophage or phagemid vector.  The antisense
     compds. were specific and effective for the elimination of target mRNA.
     Thus, the system of the present invention is used as temporary knock-down
     system to unveil functions of genes crit. for diseases.  The system of the
     present invention can be adopted not only for functional genomics but also
     for effectively validating target for antisense or other mol. therapeutics
     against various malignancies, infections, and other diseases by blocking
     specific genes involved in the disease.
REFERENCE COUNT:         13    THERE ARE 13 CITED REFERENCES AVAILABLE FOR THIS
```

RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L8 ANSWER 2 OF 15 CA COPYRIGHT 2003 ACS
ACCESSION NUMBER: 132:60106 CA
TITLE: Methods for generating highly diverse nucleic acid libraries
INVENTOR(S): Wagner, Richard; Wright, Martin C.; Kreider, Brent
PATENT ASSIGNEE(S): Phylos, Inc., USA
SOURCE: PCT Int. Appl., 32 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2000000632	A1	20000106	WO 1999-US14776	19990629
W: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, SD, SL, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
AU 9948470	A1	20000117	AU 1999-48470	19990629
EP 1092039	A1	20010418	EP 1999-932081	19990629
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI				
JP 2002519038	T2	20020702	JP 2000-557385	19990629
ZA 2000007261	A	20020515	ZA 2000-7261	20001207
NO 2000006675	A	20001228	NO 2000-6675	20001228

PRIORITY APPLN. INFO.: US 1998-90970P P 19980629
WO 1999-US14776 W 19990629

AB Disclosed herein is a method for generating a nucleic acid library. The method first involves providing a population of single-stranded nucleic acid templates, each of the templates including a coding sequence and an operably linked promoter sequence. The population of single-stranded nucleic acid templates is hybridized to a mixt. of substantially **complementary single-stranded nucleic acid** fragments, the fragments being shorter in length than the nucleic acid template. Then each of the hybridization products of the 2nd step is contacted with both a DNA polymerase which lacks strand displacement activity and a DNA ligase under conditions in which the fragments act as primers for the completion of a second nucleic acid strand which is substantially complementary to the nucleic acid template. Finally, the products of the 3rd step are contacted with RNA polymerase to generate an RNA library, the library being transcribed from the second nucleic acid strand. In preferred embodiments,the method is used to introduce one or more mutations into the library. The invention also features a method for reducing sequence variation in a population of nucleic acid mols.

REFERENCE COUNT: 10 THERE ARE 10 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L8 ANSWER 3 OF 15 MEDLINE DUPLICATE 1
ACCESSION NUMBER: 2000280072 MEDLINE
DOCUMENT NUMBER: 20280072 PubMed ID: 10773070
TITLE: Differential functional behavior of viral phi29, Nf and GA-1 SSB proteins.

AUTHOR: Gascon I; Lazaro J M; Salas M
CORPORATE SOURCE: Centro de Biologia Molecular 'Severo Ochoa' (CSIC-UAM), Universidad Autonoma, Cantoblanco, 28049-Madrid, Spain.
CONTRACT NUMBER: 2R01 GM27242-20 (NIGMS)
SOURCE: NUCLEIC ACIDS RESEARCH, (2000 May 15) 28 (10) 2034-42. Journal code: 0411011. ISSN: 1362-4962.
PUB. COUNTRY: ENGLAND: United Kingdom
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200006
ENTRY DATE: Entered STN: 20000706
Last Updated on STN: 20010521
Entered Medline: 20000626

AB DNA replication of phi29 and related phages takes place via a strand displacement mechanism, a process that generates large amounts of single-stranded DNA (ssDNA). Consequently, phage-encoded ssDNA-binding proteins (SSBs) are essential proteins during phage phi29-like DNA replication. In the present work we analyze the helix-destabilizing activity of the SSBs of phi29 and the related phages Nf and GA-1, their ability to eliminate non-productive binding of phi29 DNA polymerase to ssDNA and their stimulatory effect on replication by phi29 DNA polymerase in primed **M13** ssDNA replication, a situation that resembles type II replicative intermediates that occur during phi29-like DNA replication. Significant differences have been appreciated in the functional behavior of the three SSBs. First, the GA-1 SSB is able to display helix-destabilizing activity and to stimulate dNTP incorporation by phi29 DNA polymerase in the **M13** DNA replication assay, even at SSB concentrations at which the phi29 and Nf SSBs do not show any effect. On the other hand, the phi29 SSB is the only one of the three SSBs able to increase the replication rate of phi29 DNA polymerase in primed **M13** ssDNA replication. From the fact that the phi29 SSB, but not the Nf SSB, stimulates the replication rate of Nf DNA polymerase we conclude that the different behaviors of the SSBs on stimulation of the replication rate of phi29 and Nf DNA polymerases is most likely due to formation of different nucleoprotein complexes of the SSBs with the ssDNA rather than to a specific interaction between the SSB and the corresponding DNA polymerase. A model that correlates the thermodynamic parameters that define SSB-**ssDNA nucleoprotein complex** formation with the functional stimulatory effect of the SSB on phi29-like DNA replication has been proposed.

L8 ANSWER 4 OF 15 SCISEARCH COPYRIGHT 2003 THOMSON ISI
ACCESSION NUMBER: 2000:393645 SCISEARCH
THE GENUINE ARTICLE: 316CM
TITLE: Differential functional behavior of viral phi 29, Nf and GA-1 SSB proteins
AUTHOR: Gascon I; Lazaro J M; Salas M (Reprint)
CORPORATE SOURCE: UNIV AUTONOMA MADRID, CTR BIOL MOL SEVERO OCHOA, CSIC, UAM, E-28049 MADRID, SPAIN (Reprint); UNIV AUTONOMA MADRID, CTR BIOL MOL SEVERO OCHOA, CSIC, UAM, E-28049 MADRID, SPAIN
COUNTRY OF AUTHOR: SPAIN
SOURCE: NUCLEIC ACIDS RESEARCH, (15 MAY 2000) Vol. 28, No. 10, pp. 2034-2042.
Publisher: OXFORD UNIV PRESS, GREAT CLARENDON ST, OXFORD OX2 6DP, ENGLAND.
ISSN: 0305-1048.
DOCUMENT TYPE: Article; Journal
FILE SEGMENT: LIFE
LANGUAGE: English
REFERENCE COUNT: 54

ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

AB DNA replication of phi 29 and related phages takes place via a strand displacement mechanism, a process that generates large amounts of single-stranded DNA (ssDNA). Consequently, phage-encoded ssDNA-binding proteins (SSBs) are essential proteins during phage phi 29-like DNA replication. In the present work we analyze the helix-destabilizing activity of the SSBs of phi 29 and the related phages Nf and GA-1,their ability to eliminate non-productive binding of phi 29 DNA polymerase to ssDNA and their stimulatory effect on replication by phi 29 DNA polymerase in primed **M13** ssDNA replication, a situation that resembles type II replicative intermediates that occur during phi 29-like DNA replication. Significant differences have been appreciated in the functional behavior of the three SSBs, First, the GA-1 SSB is able to display helix-destabilizing activity and to stimulate dNTP incorporation by phi 29 DNA polymerase in the **M13** DNA replication assay, even at SSB concentrations at which the phi 29 and Nf SSBs do not show any effect, On the other hand, the phi 29 SSB is the only one of the three SSBs able to increase the replication rate of phi 29 DNA polymerase in primed **M13** ssDNA replication. From the fact that the phi 29 SSB, but not the Nf SSB, stimulates the replication rate of Nf DNA polymerase we conclude that the different behaviors of the SSBs on stimulation of the replication rate of phi 29 and Nf DNA polymerases is most likely due to formation of different nucleoprotein complexes of the SSBs with the ssDNA rather than to a specific interaction between the SSB and the corresponding DNA polymerase. A model that correlates the thermodynamic parameters that define SSB-**ssDNA nucleoprotein complex** formation with the functional stimulatory effect of the SSB on phi 29-like DNA replication has been proposed.

L8 ANSWER 5 OF 15 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.

ACCESSION NUMBER: 2000:190041 BIOSIS

DOCUMENT NUMBER: PREV200000190041

TITLE: Fluorescence and excitation Escherichia coli RecA protein spectra analyzed separately for tyrosine and tryptophan residues.

AUTHOR(S): Isaev-Ivanov, Vladimir V.; Kozlov, Mihail G.; Baitin, Dimitry M.; Masui, Ryoji; Kuramitsu, Seiki; Lanzov, Vladislav A. (1)

CORPORATE SOURCE: (1) Division of Molecular and Radiation Biophysics, Petersburg Nuclear Physics Institute, Russian Academy of Sciences, Gatchina, Saint Petersburg, 188350 Russia

SOURCE: Archives of Biochemistry and Biophysics, (April 1, 2000) Vol. 376, No. 1, pp. 124-140. ISSN: 0003-9861.

DOCUMENT TYPE: Article

LANGUAGE: English

SUMMARY LANGUAGE: English

AB The method for separation of emission (EM) and excitation (EX) spectra of a protein into EM and EX spectra of its tyrosine (Tyr) and tryptophan (Trp) residues was described. The method was applied to analysis of Escherichia coli RecA protein and its complexes with Mg2+, ATPgammaS or ADP, and single-stranded DNA (ssDNA). RecA consists of a C-terminal domain containing two Trp and two Tyr residues, a major domain with five Tyr residues, and an N-terminal domain without these residues (R. M. Story, I. T. Weber, and T. A. Steitz (1992) Nature (London) 355, 374-376). Because the fluorescence of Tyr residues in the C-terminal domain was shown to be quenched by energy transfer to Trp residues, Trp and Tyr fluorescence of RecA was provided by the C-terminal and the major domains, respectively. Spectral analysis of Trp and Tyr constituents revealed that a relative spatial location of the C-terminal and the major domains in RecA monomers was different for their complexes with either ATPgammaS or ADP, whereas this location did not change upon additional interaction of these

complexes with ssDNA. Homogeneous (that is, independent of EX wavelength) and nonhomogeneous (dependent on EX wavelength) types of Tyr and Trp fluorescence quenching were analyzed for RecA and its **complexes** with **nucleotide** cofactors and **ssDNA**. The former was expected to result from singlet-singlet energy transfer from these residues to adenine of ATPgammaS or ADP. By analogy, the latter was suggested to proceed through energy transfer from high vibrational levels of the excited state of Trp and Tyr residues to the adenine. In this case, for correct calculation of the overlap integral, Trp and Tyr donor emission spectra were substituted by the spectral function of convolution of emission and excitation spectra that resulted in a significant increase of the overlap integral and gave an explanation of the nonhomogeneous quenching of Trp residues in the C-terminal domain.

L8 ANSWER 6 OF 15 MEDLINE DUPLICATE 2
ACCESSION NUMBER: 97141743 MEDLINE
DOCUMENT NUMBER: 97141743 PubMed ID: 8988001
TITLE: Gene V protein dimerization and cooperativity of binding of poly(dA).
AUTHOR: Terwilliger T C
CORPORATE SOURCE: Structural Biology Group, Los Alamos National Laboratory, New Mexico 87545, USA.
CONTRACT NUMBER: GM38714 (NIGMS)
SOURCE: BIOCHEMISTRY, (1996 Dec 24) 35 (51) 16652-64.
Journal code: 0370623. ISSN: 0006-2960.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199701
ENTRY DATE: Entered STN: 19970219
Last Updated on STN: 19970219
Entered Medline: 19970130

AB Gene V protein of bacteriophage f1 is a dimeric protein that binds cooperatively to single-stranded nucleic acids. In order to determine whether a monomer-dimer equilibrium has an appreciable effect upon the thermodynamics of gene V protein binding to nucleic acids, the dissociation constant for the protein dimer was investigated using size-exclusion chromatography. At concentrations ranging from 5 x 10(-10) to 1.2 x 10(-5) M, the Stokes radius of the protein was that expected of the dimer of the gene V protein. The Stokes radius of the protein was also independent of salt concentration from 0.2 to 1.0 M NaCl in a buffer containing 10 mM Tris-HCl, pH 7.4, and 1 mM EDTA. The binding of the dimeric gene V protein to poly(dA) was studied using a simplified lattice model for protein-protein interactions adapted for use with a dimeric protein that binds simultaneously to two strands of nucleic acid. Interpretation of the salt dependence, C = [d log(Kint omega)]/[d log(NaCl)], of binding of such a dimeric protein to nucleic acid using the theory of Record et al. (Record, M. T., et al. (1976) J. Mol. Biol. 107, 145-158) indicates that C is a function of the numbers of cations and anions released from protein and nucleic acid upon binding of the dimer, not of the monomer. Cooperativity of gene V protein binding to poly(dA) was studied with titration experiments that are sensitive to the degree of cooperativity of binding. The cooperativity factor omega, defined as the ratio of the binding constant for a site adjacent to a previously bound dimer to that for an isolated site, was found to be relatively insensitive to salt, with a value in the range of 2000-7000 for binding to poly(dA) at 3 degrees C and at 23 degrees C. This high cooperativity factor supports the suggestion that protein-protein contacts play a major role in the formation of the superhelical gene V protein-**single-stranded nucleic acid complex**.

L8 ANSWER 7 OF 15 CA COPYRIGHT 2003 ACS
ACCESSION NUMBER: 123:105487 CA
TITLE: Kinetic Studies by Fluorescence Resonance Energy Transfer Employing a Double-Labeled Oligonucleotide: Hybridization to the **Oligonucleotide Complement** and to **Single-Stranded DNA**
AUTHOR(S): Parkhurst, Kay M.; Parkhurst, Lawrence J.
CORPORATE SOURCE: Department of Chemistry, University of Nebraska Lincoln, Lincoln, NE, 68588-0304, USA
SOURCE: Biochemistry (1995), 34(1), 285-92
CODEN: BICHAW; ISSN: 0006-2960
PUBLISHER: American Chemical Society
DOCUMENT TYPE: Journal
LANGUAGE: English

AB A single 16-base oligodeoxyribonucleotide was labeled at the 3'-end with fluorescein and at the 5'-end with x-rhodamine (R*oligo*F); the chromophores served as a donor/acceptor pair, resp., for Forster resonance energy transfer. We exploited the striking differences in the steady-state emission spectra of the R*oligo*F as a single strand and in a duplex structure to signal hybridization in soln. and to det. the kinetics of duplex formation as the probe bound to its oligomer complement and to its target sequence in M13mp18(+) phage DNA. The binding followed second-order kinetics; in 0.18 M NaCl (pH 8) with 25% formamide, the rate const. for binding to the oligomer complement was 5.7 .times. 105 M-1 s-1, and that to M13mp18(+) was 5.7 .times. 104 M-1 s-1. The source of the 10-fold decrease in the rate of binding to M13mp18(+) was examd. to differentiate between multiple nonproductive nucleation and rapid fluctuations in the structure around the target site. From simulations based on each model combined with assocd. exptl. results, we concluded that the slower binding was due to rapid structural fluctuations around the target site, with an effective target concn. 0.1 of that of the total. Comparisons of total fluorescein emission derived from both steady-state and lifetime measurements suggest that the 5'-x-rhodamine induces a conformational change that affects the interaction at the 3'-end between the fluorescein and the polymer. The effects of salt on the fluorescence were complex. The static quenching of fluorescein in the single-labeled, single-stranded oligonucleotide did not change with NaCl (0-0.18 M), whereas there were marked changes in the double-labeled probe, showing that the conformational effects mediated by the 5'-x-rhodamine were salt dependent.

L8 ANSWER 8 OF 15 MEDLINE DUPLICATE 3
ACCESSION NUMBER: 95082803 MEDLINE
DOCUMENT NUMBER: 95082803 PubMed ID: 7990840
TITLE: [A new method of covalent immobilization of oligodeoxyribonucleotides on nylon membranes for hybridization with nucleic acids].
Novyi metod kovalentnoi immobilizatsii oligodezoksiribonukleotidov na neilonovykh membranakh dlia gibridizatsii s nukleinovymi kislotami.
AUTHOR: Ivanovskaia M G; Kozlov I A; Lebedeva I V; Shabarova Z A
SOURCE: MOLEKULIARNAIA BIOLOGIIA, (1994 Sep-Oct) 28 (5) 1176-82.
Journal code: 0105454. ISSN: 0026-8984.
PUB. COUNTRY: RUSSIA: Russian Federation
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: Russian
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199501
ENTRY DATE: Entered STN: 19950124
Last Updated on STN: 19950124
Entered Medline: 19950112

AB A new method of covalent immobilization of oligodeoxyribonucleotides on nylon membranes which contain surface amino groups was developed. The method consists in condensation between the amino group of the membrane and the carboxyl group of modified oligonucleotide by means of 1-ethyl-3-(3'-dimethylaminopropyl)carbodiimide. The carboxyl group was introduced into the oligonucleotide by means of postsynthetic attachment of peptide (reduced glutathione) at the terminal phosphate group of the oligonucleotide, using the N-hydroxybenzotriazole method of phosphate activation. Membranes containing a covalently immobilized 23-membered oligonucleotide were tested in hybridization with **complementary oligonucleotide**, and with **single-stranded DNA** of bacteriophage **M13** which has a complementary sequence. The method of covalent immobilization is very simple and convenient. The membranes with covalently immobilized oligonucleotides may be used not only in hybridization analysis, but also for purification of nucleic acids and proteins which recognize nucleotide sequences and in sense biotechnology.

L8 ANSWER 9 OF 15 SCISEARCH COPYRIGHT 2003 THOMSON ISI
ACCESSION NUMBER: 95:191195 SCISEARCH
THE GENUINE ARTICLE: QL239
TITLE: NEW METHOD FOR COVALENT IMMOBILIZATION OF OLIGONUCLEOTIDES ON NYLON MEMBRANES
AUTHOR: IVANOVSKAYA M G (Reprint); KOZLOV I A; LEBEDEVA I V; SHABAROVA Z A
CORPORATE SOURCE: MOSCOW MV LOMONOSOV STATE UNIV, BELOZERSKII INST PHYSICOCHEM BIOL, MOSCOW 119899, RUSSIA (Reprint)
COUNTRY OF AUTHOR: RUSSIA
SOURCE: MOLECULAR BIOLOGY, (SEP/OCT 1994) Vol. 28, No. 5, Part 2, pp. 754-756.
ISSN: 0026-8933.
DOCUMENT TYPE: Article; Journal
FILE SEGMENT: LIFE
LANGUAGE: ENGLISH
REFERENCE COUNT: 6

ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

AB An efficient method was developed for covalent immobilization of oligodeoxyribonucleotides on commercially available nylon membranes containing amino groups. It is based on condensation of the membrane amino groups with the oligonucleotide carboxyls in the presence of 1-ethyl-3-(3'-dimethylaminopropyl)carbodiimide. Membranes containing an immobilized 23-membered oligonucleotide were hybridized with a **complementary oligonucleotide** and **single-stranded M13 DNA**. The membranes obtained could be used for hybridization analysis and isolation of nucleic acids and proteins recognizing certain sequences.

L8 ANSWER 10 OF 15 CA COPYRIGHT 2003 ACS
ACCESSION NUMBER: 113:94357 CA
TITLE: Methods for detecting nucleic acid sequences
INVENTOR(S): Duck, Peter; Bender, Robert
PATENT ASSIGNEE(S): Meiogenics, Inc., USA
SOURCE: PCT Int. Appl., 34 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 2
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 8910415	A1	19891102	WO 1989-US1825	19890428

W: AU, DK, JP
RW: AT, BE, CH, DE, FR, GB, IT, LU, NL, SE

US 5011769	A	19910430	US 1988-187814	19880429
AU 8935697	A1	19891124	AU 1989-35697	19890428
EP 365663	A1	19900502	EP 1989-905902	19890428
R: AT, BE, CH, DE, FR, GB, IT, LI, LU, NL, SE				
JP 02504110	T2	19901129	JP 1989-505932	19890428
JP 2839608	B2	19981216		
DK 8906658	A	19900202	DK 1989-6658	19891222
PRIORITY APPLN. INFO.:			US 1988-187814	19880429
			US 1985-805279	19851205
			WO 1989-US1825	19890428

AB Target nucleic acid sequences are detected by (a) forming a reaction mixt. which includes the target and an amt. of a **complementary single-stranded nucleic acid** probe which is greater than the target under conditions which allow the probe and target to hybridize; (b) nicking the hybridized probe at least once within a predetd. sequence to form .gtoreq.2 probe fragments hybridized to the target, resulting in the probe fragments becoming single-stranded and allowing the target nucleic acid to hybridize to another probe; (c) identifying the probe fragments, thereby detecting the target nucleic acid. The probe comprises [NA1RNA2]n (NA1, NA2 = nucleic acid sequences; R = RNA sequence; n = 1-10) and is nicked with a double-stranded RNase. Probes [e.g. 5'-d(CCAGGGTT)r(UUCCC)d(AGTCACG)3'] were labeled with [32P]-ATP and incubated with target DNA at 65.degree. for 10 min and at 37.degree. for 30 min. RNase H was then added at 0, 10, and 20 min. After 30 min the mixt. was loaded with formamide dye on a 0.8 mm 20% acrylamide/7 M urea gel at 800 V with a heating plate. The sensitivity was ~10-19-10-20 mol target.

L8 ANSWER 11 OF 15 MEDLINE DUPLICATE 4

ACCESSION NUMBER:	88224566 MEDLINE
DOCUMENT NUMBER:	88224566 PubMed ID: 3286164
TITLE:	Site-specific oligonucleotide-directed mutagenesis using T4 DNA polymerase.
AUTHOR:	Chang G J; Johnson B J; Trent D W
CORPORATE SOURCE:	Division of Vector-Borne Viral Diseases, Centers for Disease Control, Fort Collins, CO 80522.
SOURCE:	DNA, (1988 Apr) 7 (3) 211-7. Journal code: 8302432. ISSN: 0198-0238.
PUB. COUNTRY:	United States
DOCUMENT TYPE:	Journal; Article; (JOURNAL ARTICLE)
LANGUAGE:	English
FILE SEGMENT:	Priority Journals
ENTRY MONTH:	198806
ENTRY DATE:	Entered STN: 19900308 Last Updated on STN: 19980206 Entered Medline: 19880627

AB A simple and efficient mutagenesis procedure is described which uses both the 3'----5' exonuclease and 5'----3' polymerase activities of T4 DNA polymerase. Different types of mutation-deletion, insertion, and substitution-can be introduced into the DNA in a single reaction. The technique uses recombinant **M13 single-stranded DNA** and two **complementary** DNA **oligonucleotides** to target and control the extent of deletions catalyzed by T4 DNA polymerase. The second oligonucleotide not only directs ligation, but also serves as a template for insertion or substitution of nucleotides by T4 polymerase. Mutant phages in a genetically pure form can be obtained at high efficiency, allowing their characterization directly by nucleotide sequencing without prior enrichment, plaque purification, and screening. We tested the versatility of this method by manipulating five regions of cDNA encoding the structural proteins of eastern equine encephalitis

virus.

L8 ANSWER 12 OF 15 MEDLINE DUPLICATE 5
ACCESSION NUMBER: 88062759 MEDLINE
DOCUMENT NUMBER: 88062759 PubMed ID: 3316669
TITLE: Solution hybridization of crosslinkable DNA oligonucleotides to bacteriophage **M13** DNA. Effect of secondary structure on hybridization kinetics and equilibria.
AUTHOR: Gamper H B; Cimino G D; Hearst J E
CORPORATE SOURCE: HRI Research Incorporated, Berkeley, CA 94710.
CONTRACT NUMBER: GM 11180 (NIGMS)
SOURCE: JOURNAL OF MOLECULAR BIOLOGY, (1987 Sep 20) 197 (2) 349-62. Journal code: 2985088R. ISSN: 0022-2836.
PUB. COUNTRY: ENGLAND: United Kingdom
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 198801
ENTRY DATE: Entered STN: 19900305
Last Updated on STN: 19970203
Entered Medline: 19880112

AB Several DNA oligonucleotides have been photochemically modified with the furocoumarin 4'-hydroxymethyl-4,5',8-trimethylpsoralen (HMT) such that each contained a single HMT furan side monoadduct to thymidine at a unique 5' TpA 3' sequence. When these oligonucleotides were hybridized to their respective complements, the HMT adduct could be driven to form an interstrand crosslink by irradiation of the hybrid with 360 nm light. The ability to crosslink probe-target complexes has allowed us to determine the kinetics and the extent of hybridization in solution between these **oligonucleotides** and their **complementary** sequences in **single-stranded** bacteriophage **M13 DNA** . Our data indicate that these parameters are strongly influenced by the existence of local as well as global secondary structure in the viral DNA. During hybridization, rearrangement of this secondary structure so as to expose the target sequence can be rate-limiting. Upon attainment of equilibrium, only a portion of the target sequence may be hybridized to the probe with the remainder involved in intrastrand base-pairing. Using crosslinkable oligonucleotide probes hybridized and irradiated near the melting temperature of the respective probe-target complex one can partially overcome these secondary structure effects.

L8 ANSWER 13 OF 15 CA COPYRIGHT 2003 ACS
ACCESSION NUMBER: 107:3125 CA
TITLE: Restriction of single-stranded **M13** DNA using synthetic oligonucleotides: the structural requirement of restriction enzymes
AUTHOR(S): Qi, Guorong; Wong, Pierre; Cedergren, Robert
CORPORATE SOURCE: Dep. Biochem., Univ. Montreal, Montreal, QC, H3C 3J7, Can.
SOURCE: Biochemistry and Cell Biology (1987), 65(1), 50-5 CODEN: BCBIEQ; ISSN: 0829-8211
DOCUMENT TYPE: Journal
LANGUAGE: English

AB A targeted ss (single-stranded) DNA cleavage technique is reported which involves the use of a synthetic oligomers complementary to the ss **M13** DNA polylinker. BamH1, SmaI, And KpnI restriction enzymes were tested with a partial duplex DNA formed from ss **M13** DNA and a nested series of fragments derived from a synthetic 21-mer which were complementary to the polylinker region. These enzymes require .ltoreq.2 flanking nucleotides in addn. to the hexameric recognition site for efficient cleavage. Thus, this technique could be useful for effecting

unique cleavages of DNA with enzymes which generally give a large no. of fragments and for strategies of ss DNA manipulation.

L8 ANSWER 14 OF 15 MEDLINE DUPLICATE 6
ACCESSION NUMBER: 85191078 MEDLINE
DOCUMENT NUMBER: 85191078 PubMed ID: 3991809
TITLE: A rapid single-stranded cloning strategy for producing a sequential series of overlapping clones for use in DNA sequencing: application to sequencing the corn mitochondrial 18 S rDNA.
AUTHOR: Dale R M; McClure B A; Houchins J P
CONTRACT NUMBER: 5T32 GM07094 (NIGMS)
GM32113 (NIGMS)
SOURCE: PLASMID, (1985 Jan) 13 (1) 31-40.
Journal code: 7802221. ISSN: 0147-619X.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-M10248
ENTRY MONTH: 198506
ENTRY DATE: Entered STN: 19900320
Last Updated on STN: 19970203
Entered Medline: 19850612
AB A simple new procedure was described for producing a sequential series of overlapping clones for use in DNA sequencing. The technique used **single-stranded M13 DNA** and **complementary** DNA **oligomers** to form specific cleavage and ligation substrates. It was, therefore, independent of the sequence of the DNA cloned into the vector. Deletions of varying sizes were generated from one end of the insert through the 3' to 5' exonuclease activity of T4 DNA polymerase. The approximate size of the deletion and therefore the starting point for DNA sequencing could be estimated by electrophoresis of the subcloned phage DNA on a agarose gel. This greatly reduced the number of templates that must be sequenced to obtain a complete sequence. The entire procedure could be carried out in one tube in less than a day. The procedure was used to subclone and sequence the maize mitochondrial 18 S rDNA and 5' flanking region (2622 bases) in less than a week. Other applications of oligomers and single-stranded DNA in the construction of insertions, deletions, and cDNAs are discussed.

L8 ANSWER 15 OF 15 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.DUPLICATE 7
ACCESSION NUMBER: 1985:351769 BIOSIS
DOCUMENT NUMBER: BA80:21761
TITLE: THE ORIGIN OF THE HELPER COMPONENT OF TOBACCO VEIN MOTTLING VIRUS TRANSLATIONAL INITIATION NEAR THE 5' TERMINUS OF THE VIRAL RNA AND TERMINATION BY UAG CODONS.
AUTHOR(S): HELLMANN G M; SHAW J G; RHOADS R E
CORPORATE SOURCE: DEP. BIOCHEM., UNIV. KY., LEXINGTON, KY. 40536.
SOURCE: VIROLOGY, (1985) 143 (1), 23-34.
CODEN: VIRLAX. ISSN: 0042-6822.
FILE SEGMENT: BA; OLD
LANGUAGE: English
AB The nature of the polypeptide products encoded by the 5'-terminal region of the RNA of the potyvirus, tobacco vein mottling virus (TVMV), was investigated. **Single-stranded DNA** probes **complementary** to either **nucleotides** 1100-2100 or 2100-2820 from the 5' terminus of the RNA were prepared by subcloning recombinant plasmids in bacteriophage **M13**. These were hybridized to TVMV RNA, the DNA:RNA hybrids translated in a reticulocyte lysate cell-free translation system (hybrid-arrested translation), and the

products analyzed by electrophoresis on sodium dodecyl sulfate-containing polyacrylamide gels. The hybrids produced altered patterns of polypeptides which indicated that the major products, P75, was translated from the 5' terminus of the RNA. The N-terminal portion (MW .apprx. 35,000) of P75 did not react with antisera to any of the 5 known potyviral protein, suggesting the existence of a previously unidentified cistron at the 5' terminus. Translation of additional RNA sequences produced a polypeptide with a MW of 68,000 which was immunoprecipitable by antiserum to TVMV helper component, establishing the coding region for helper component near the 5' terminus. Limited DNA sequence analysis of the region encoding the C terminus of P75 revealed an open reading frame of 369 nucleotides followed by a pair of UAG codons. Pulse-chase experiments demonstrated that in the first 10 min of incubation, the only polypeptidase initiated was P75, suggesting that products downstream from P75 arose from in vitro fragmentation of TVMV RNA and translation of the RNA fragments.

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=> d his

     (FILE 'HOME' ENTERED AT 13:02:29 ON 26 MAY 2003)

     FILE 'MEDLINE, BIOSIS, EMBASE, CA, SCISEARCH' ENTERED AT 13:02:49 ON 26
     MAY 2003
L1        101549 S ANTISENSE OR (COMPLE (2N) (OLIGO? OR NUCLEI?))
L2        217407 S ANTISENSE? OR (COMPLE? (2N) (OLIGO? OR NUCLE?))
L3         77824 S SSDNA OR (SINGL? STRAND? (2N) (DNA OR RNA OR (NUCLE? ACID?)))
L4          4019 S L2 AND L3
L5           603 S L2 (5N) L3
L6           474 S L2 (3N) L3
L7            26 S L6 AND M13
L8            15 DUP REM L7 (11 DUPLICATES REMOVED)

=> s antisense or (comple (2n) (oligo? or nucle?))
<------User Break------>

SEARCH ENDED BY USER
SEARCH ENDED BY USER

=> s antisense or (complem? (2n) (oligo? or nucle?))
<------User Break------>

SEARCH ENDED BY USER
SEARCH ENDED BY USER

=> s antisense? or (complem? (2n) (oligo? or nucle?))
L9       123487 ANTISENSE? OR (COMPLEM? (2N) (OLIGO? OR NUCLE?))

=> s antisense? or (anti (n) sense) or (complem? (2n) (oligo? or nucle?))
L10      126636 ANTISENSE? OR (ANTI (N) SENSE) OR (COMPLEM? (2N) (OLIGO? OR
                NUCLE?))

=> s l10 and m13
L11          231 L10 AND M13

=> s l10 (2n) m 13
L12            1 L10 (2N) M 13

=> s l10 (2n) m13
L13            9 L10 (2N) M13

=> dup rem l13
PROCESSING COMPLETED FOR L13
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L14 6 DUP REM L13 (3 DUPLICATES REMOVED)

=> d l14 1-6 ibib abs

L14 ANSWER 1 OF 6 CA COPYRIGHT 2003 ACS
ACCESSION NUMBER: 137:364368 CA
TITLE: Libraries of RNAs that can be prepared as large circular molecules and their use in high throughput screening and functional genomics
INVENTOR(S): Park, Jong-Gu; Moon, Ik-Jae; Lee, Yun-Han
PATENT ASSIGNEE(S): Welgene, Inc., S. Korea
SOURCE: PCT Int. Appl., 87 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 2
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2002092808	A1	20021121	WO 2002-IB735	20020309

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG

PRIORITY APPLN. INFO.: KR 2001-27071 A 20010517
AB The present invention provides a high-throughput system for functional genomics using a random gene unidirectional antisense library comprising large circular RNAs including on or more an antisense segments. The antisense RNAs are specific and effective inhibitors of translation of a target mRNA. Thus, the system may be effectively used as temporary knock-down system to unveil functions of genes crit. for diseases. The RNA sequences are obtained from a specific biol. state, such as a disease state, by methods such as subtractive hybridization. The selected sequences may then be used to selectively inhibit state-specific genes. These large sequences are generated from bacteriophage or phagemid clones and because they may be several hundred or thousand base pairs long, they are accurate and specific in their effects. Use of bacteriophage M13 and phagemids to generate large circular RNAs inhibiting expression of genes for tumor necrosis factor .alpha. and NF-.kappa.B is demonstrated. The system of the present invention can be adapted not only for functional genomics but also for effectively validating target for antisense or other mol. therapeutics against various malignancies, infections, and other diseases by blocking specific genes involved in the disease.
REFERENCE COUNT: 9 THERE ARE 9 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L14 ANSWER 2 OF 6 CA COPYRIGHT 2003 ACS
ACCESSION NUMBER: 134:142799 CA
TITLE: Plasmodium falciparum carbamoyl phosphate synthetase II gene sequence and production of ribozymes, antisense molecules and other gene inactivation agents designed from this sequence
INVENTOR(S): Stewart, Thomas S.; Flores, Maria V.; O'sullivan, William J.
PATENT ASSIGNEE(S): Unisearch Ltd., Australia

SOURCE: U.S., 32 pp., Cont.-in-part of U.S. 5,849,573.
CODEN: USXXAM
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 2
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 6183996	B1	20010206	US 1998-150741	19980910
WO 9412643	A1	19940609	WO 1993-AU617	19931202
W: AT, AU, BB, BG, BR, BY, CA, CH, CZ, DE, DK, ES, FI, GB, HU, JP, KP, KR, KZ, LK, LU, LV, MG, MN, MW, NL, NO, NZ, PL, PT, RO, RU, SD, SE, SK, UA, US, UZ, VN				
RW: AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG				
ZA 9309080	A	19940805	ZA 1993-9080	19931203
US 5849573	A	19981215	US 1995-446855	19950706

PRIORITY APPLN. INFO.:
AU 1992-6206 A 19921203
AU 1992-6380 A 19921216
WO 1993-AU617 W 19931202
US 1995-446855 A2 19950706

AB The present invention provides a nucleotide sequence encoding carbamoyl phosphate synthetase II of Plasmodium falciparum. Carbamoyl phosphate synthetase II catalyzes the first committed and rate-limiting step in the de novo pyrimidine biosynthetic pathway. P. falciparum relies exclusively on pyrimidine synthesis de novo because of its inability to salvage pyrimidines. Mature human red blood cells, however, have no recognized requirement for a pyrimidine nucleotide. Accordingly, this enzyme represents a prime chemotherapeutic locus. The present invention relates to the use of the sequence encoding carbamoyl phosphate synthetase II in the recombinant prodn. of carbamoyl phosphate synthetase II and to antisense mols., ribozymes and other gene inactivation agents designed from this sequence.

REFERENCE COUNT: 15 THERE ARE 15 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L14 ANSWER 3 OF 6 CA COPYRIGHT 2003 ACS
ACCESSION NUMBER: 119:242934 CA
TITLE: Photocleavage of DNA using organic oxyradicals
INVENTOR(S): Herkstroeter, William George; Farid, Samir Yacoub; Gould, Ian Robert; Chen, Chin Hsin; Jayaraman, Krishna; Specht, Donald P.
PATENT ASSIGNEE(S): Eastman Kodak Co., USA
SOURCE: PCT Int. Appl., 56 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9314104	A1	19930722	WO 1993-US256	19930113
W: CA, JP				
RW: AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE				

PRIORITY APPLN. INFO.:
US 1992-819905 19920113
US 1993-1362 19930107

OTHER SOURCE(S): MARPAT 119:242934

AB Compns. for photocleavage of DNA comprise an oligonucleotide conjugated to an org. oxyradical precursor. The precursor can produce an oxyradical by direct photoexcitation, or by accepting an electron from a dye followed by

release of an oxyradical. Upon exposure of a soln. contg. the target DNA and the conjugate (and a dye if necessary) to activating light, an oxyradical is produced and the sugar-phosphate backbone of the target is cleaved. Alternatively, the oligonucleotide can be conjugated to the dye. A conjugate of acridine orange and **M13-complementary oligonucleotide** was prepd. Exposure of a soln. of M13, dye-oligonucleotide conjugate, and oxyradical precursor 1,5-bis-(stilbazole-N-oxide)-pentane to light of appropriate wavelength resulted in cleavage of M13 in only one confined region of the entire DNA sequence.

L14 ANSWER 4 OF 6 CA COPYRIGHT 2003 ACS
ACCESSION NUMBER: 114:1791 CA
TITLE: Detection of nucleic acid sequences using particle agglutination
INVENTOR(S): Olson, Jeffrey C.
PATENT ASSIGNEE(S): Angenics, Inc., USA
SOURCE: PCT Int. Appl., 64 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9002205	A1	19900308	WO 1989-US3624	19890823

W: JP
RW: AT, BE, CH, DE, FR, GB, IT, LU, NL, SE
PRIORITY APPLN. INFO.: US 1988-236535 19880825
AB A target nucleic acid in a sample is detected using .gtoreq.2 noncomplementary nucleic acid probes which can hybridize to two nonoverlapping areas of the target sequence, these probes are labeled with .gtoreq.1 mol. of one member of a specific binding pair, and with particles carrying the 2nd member of the specific binding pair and allowing the probes to hybridize with the target nucleic acid. The target nucleic acid hybridized to the two oligonucleotide probes are then bound by the particles with the formation of crosslinked aggregates. This agglutination can be detected. Two different 15-residue **oligonucleotides** which were **complementary** to **M13** mp18 DNA and which were biotinylated were added to M13mp18. Biotinylated DNA was produced by the polymerase chain reaction. This amplified DNA was added to streptavidin-or avidin-latex conjugates. The presence of the M13mp18 target DNA was indicated by agglutination of the latex particles.

L14 ANSWER 5 OF 6 MEDLINE DUPLICATE 1
ACCESSION NUMBER: 90076481 MEDLINE
DOCUMENT NUMBER: 90076481 PubMed ID: 2480250
TITLE: The algorithm of estimation of the Km values for primers of various structure and length in the polymerization reaction catalyzed by Klenow fragment of DNA polymerase I from E. coli.
AUTHOR: Nevinsky G A; Nemudraya A V; Levina A S; Khomov V V
CORPORATE SOURCE: Novosibirsk Institute of Bioorganic Chemistry, Siberian Division of the USSR Academy of Sciences, Novosibirsk.
SOURCE: FEBS LETTERS, (1989 Nov 20) 258 (1) 166-70.
Journal code: 0155157. ISSN: 0014-5793.
PUB. COUNTRY: Netherlands
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199001

ENTRY DATE: Entered STN: 19900328
Last Updated on STN: 19980206
Entered Medline: 19900123

AB DNA synthesis at primers d(pT)n, d(pA)n, d(pC)n, and d(pG)n in the presence of corresponding complementary templates and at hetero-**oligoprimers complementary** to **M13** phage DNA was investigated. The values of both -log Km and log Vmax increased linearly if homo-oligoprimers contained less than 10 nucleotides. The lengthening of d(pT)n and d(pA)n primers by one mononucleotide unit (n = 1-10) resulted in the 1.82-fold decrease of the Km values. The incremental decreases of Km for d(pC)n and d(pG)n were equal to about 2.46. The enhancement of the homo- and hetero-oligonucleotide primers' affinity to the enzyme due to one Watson-Crick hydrogen bond between complementary template and primer is about 1.35 times. This allows to calculate the Km values for primers of various structure and length up to 10 units. The objective laws of the Km and Vmax values changes for primers containing more than 10 nucleotides were analyzed.

L14 ANSWER 6 OF 6 MEDLINE DUPLICATE 2
ACCESSION NUMBER: 85191078 MEDLINE
DOCUMENT NUMBER: 85191078 PubMed ID: 3991809
TITLE: A rapid single-stranded cloning strategy for producing a sequential series of overlapping clones for use in DNA sequencing: application to sequencing the corn mitochondrial 18 S rDNA.
AUTHOR: Dale R M; McClure B A; Houchins J P
CONTRACT NUMBER: 5T32 GM07094 (NIGMS)
GM32113 (NIGMS)
SOURCE: PLASMID, (1985 Jan) 13 (1) 31-40.
Journal code: 7802221. ISSN: 0147-619X.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-M10248
ENTRY MONTH: 198506
ENTRY DATE: Entered STN: 19900320
Last Updated on STN: 19970203
Entered Medline: 19850612

AB A simple new procedure was described for producing a sequential series of overlapping clones for use in DNA sequencing. The technique used single-stranded **M13** DNA and **complementary** DNA **oligomers** to form specific cleavage and ligation substrates. It was, therefore, independent of the sequence of the DNA cloned into the vector. Deletions of varying sizes were generated from one end of the insert through the 3' to 5' exonuclease activity of T4 DNA polymerase. The approximate size of the deletion and therefore the starting point for DNA sequencing could be estimated by electrophoresis of the subcloned phage DNA on a agarose gel. This greatly reduced the number of templates that must be sequenced to obtain a complete sequence. The entire procedure could be carried out in one tube in less than a day. The procedure was used to subclone and sequence the maize mitochondrial 18 S rDNA and 5' flanking region (2622 bases) in less than a week. Other applications of oligomers and single-stranded DNA in the construction of insertions, deletions, and cDNAs are discussed.

=> d his

(FILE 'HOME' ENTERED AT 13:02:29 ON 26 MAY 2003)

FILE 'MEDLINE, BIOSIS, EMBASE, CA, SCISEARCH' ENTERED AT 13:02:49 ON 26

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     MAY 2003
L1        101549 S ANTISENSE OR (COMPLE (2N) (OLIGO? OR NUCLEI?))
L2        217407 S ANTISENSE? OR (COMPLE? (2N) (OLIGO? OR NUCLE?))
L3         77824 S SSDNA OR (SINGL? STRAND? (2N) (DNA OR RNA OR (NUCLE? ACID?)))
L4          4019 S L2 AND L3
L5           603 S L2 (5N) L3
L6           474 S L2 (3N) L3
L7            26 S L6 AND M13
L8            15 DUP REM L7 (11 DUPLICATES REMOVED)
L9        123487 S ANTISENSE? OR (COMPLEM? (2N) (OLIGO? OR NUCLE?))
L10       126636 S ANTISENSE? OR (ANTI (N) SENSE) OR (COMPLEM? (2N) (OLIGO? OR N
L11          231 S L10 AND M13
L12            1 S L10 (2N) M 13
L13            9 S L10 (2N) M13
L14            6 DUP REM L13 (3 DUPLICATES REMOVED)

=> s l3 and m13
L15        2854 L3 AND M13

=> s l15 and l10
L16          69 L15 AND L10

=> s l16 and (circ? (5n) l10)
L17           1 L16 AND (CIRC? (5N) L10)

=> d l17 ibib abs

L17  ANSWER 1 OF 1  CA  COPYRIGHT 2003 ACS
ACCESSION NUMBER:         137:380940  CA
TITLE:                    Unigene unidirectional antisense library
                          derived from recombinant bacteriophage or phagemid
                          vector for therapy and massive functional genomics
INVENTOR(S):              Park, Jong-Gu; Moon, Ik-Jae; Lee, Yun-Han
PATENT ASSIGNEE(S):       Welgene Pharmaceuticals, Inc., S. Korea
SOURCE:                   PCT Int. Appl., 79 pp.
                          CODEN: PIXXD2
DOCUMENT TYPE:            Patent
LANGUAGE:                 English
FAMILY ACC. NUM. COUNT:   2
PATENT INFORMATION:

     PATENT NO.        KIND  DATE          APPLICATION NO.  DATE
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     WO 2002092807      A1   20021121      WO 2002-IB1753   20020516
         W:  AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN,
             CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH,
             GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR,
             LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH,
             PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ,
             UA, UG, US, UZ, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU,
             TJ, TM
         RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, CH,
             CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR,
             BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG
PRIORITY APPLN. INFO.:                    KR 2001-27071    A  20010517
AB   The present invention provides a high throughput system for functional
     genomics using a unigene antisense library comprising large
     circular (LC)-antisense compds.  The said large
     circular (LC)-antisense compds are derived from
     recombinant bacteriophage or phagemid vector.  The antisense
     compds. were specific and effective for the elimination of target mRNA.
     Thus, the system of the present invention is used as temporary knock-down
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system to unveil functions of genes crit. for diseases. The system of the present invention can be adopted not only for functional genomics but also for effectively validating target for **antisense** or other mol. therapeutics against various malignancies, infections, and other diseases by blocking specific genes involved in the disease.
REFERENCE COUNT: 13 THERE ARE 13 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

=> d his

(FILE 'HOME' ENTERED AT 13:02:29 ON 26 MAY 2003)

FILE 'MEDLINE, BIOSIS, EMBASE, CA, SCISEARCH' ENTERED AT 13:02:49 ON 26 MAY 2003
L1 101549 S ANTISENSE OR (COMPLE (2N) (OLIGO? OR NUCLEI?))
L2 217407 S ANTISENSE? OR (COMPLE? (2N) (OLIGO? OR NUCLE?))
L3 77824 S SSDNA OR (SINGL? STRAND? (2N) (DNA OR RNA OR (NUCLE? ACID?)))
L4 4019 S L2 AND L3
L5 603 S L2 (5N) L3
L6 474 S L2 (3N) L3
L7 26 S L6 AND M13
L8 15 DUP REM L7 (11 DUPLICATES REMOVED)
L9 123487 S ANTISENSE? OR (COMPLEM? (2N) (OLIGO? OR NUCLE?))
L10 126636 S ANTISENSE? OR (ANTI (N) SENSE) OR (COMPLEM? (2N) (OLIGO? OR N
L11 231 S L10 AND M13
L12 1 S L10 (2N) M 13
L13 9 S L10 (2N) M13
L14 6 DUP REM L13 (3 DUPLICATES REMOVED)
L15 2854 S L3 AND M13
L16 69 S L15 AND L10
L17 1 S L16 AND (CIRC? (5N) L10)

=> s (circ? (5n) l10)
L18 186 (CIRC? (5N) L10)

=> s l18 and m13
L19 3 L18 AND M13

=> dup rem l19
PROCESSING COMPLETED FOR L19
L20 3 DUP REM L19 (0 DUPLICATES REMOVED)

=> d l20 1-3 ibib abs

L20 ANSWER 1 OF 3 CA COPYRIGHT 2003 ACS
ACCESSION NUMBER: 137:364368 CA
TITLE: Libraries of RNAs that can be prepared as large circular molecules and their use in high throughput screening and functional genomics
INVENTOR(S): Park, Jong-Gu; Moon, Ik-Jae; Lee, Yun-Han
PATENT ASSIGNEE(S): Welgene, Inc., S. Korea
SOURCE: PCT Int. Appl., 87 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 2
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2002092808	A1	20021121	WO 2002-IB735	20020309

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM

RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG

PRIORITY APPLN. INFO.: KR 2001-27071 A 20010517

AB The present invention provides a high-throughput system for functional genomics using a random gene unidirectional **antisense** library comprising large **circular** RNAs including on or more an antisense segments. The antisense RNAs are specific and effective inhibitors of translation of a target mRNA. Thus, the system may be effectively used as temporary knock-down system to unveil functions of genes crit. for diseases. The RNA sequences are obtained from a specific biol. state, such as a disease state, by methods such as subtractive hybridization. The selected sequences may then be used to selectively inhibit state-specific genes. These large sequences are generated from bacteriophage or phagemid clones and because they may be several hundred or thousand base pairs long, they are accurate and specific in their effects. Use of bacteriophage **M13** and phagemids to generate large circular RNAs inhibiting expression of genes for tumor necrosis factor .alpha. and NF-.kappa.B is demonstrated. The system of the present invention can be adapted not only for functional genomics but also for effectively validating target for antisense or other mol. therapeutics against various malignancies, infections, and other diseases by blocking specific genes involved in the disease.

REFERENCE COUNT: 9 THERE ARE 9 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L20 ANSWER 2 OF 3 CA COPYRIGHT 2003 ACS

ACCESSION NUMBER: 137:380940 CA

TITLE: Unigene unidirectional antisense library derived from recombinant bacteriophage or phagemid vector for therapy and massive functional genomics

INVENTOR(S): Park, Jong-Gu; Moon, Ik-Jae; Lee, Yun-Han

PATENT ASSIGNEE(S): Welgene Pharmaceuticals, Inc., S. Korea

SOURCE: PCT Int. Appl., 79 pp.
CODEN: PIXXD2

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 2

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2002092807	A1	20021121	WO 2002-IB1753	20020516

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM

RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG

PRIORITY APPLN. INFO.: KR 2001-27071 A 20010517

AB The present invention provides a high throughput system for functional

genomics using a unigene **antisense** library comprising large **circular** (LC)-**antisense** compds. The said large **circular** (LC)-**antisense** compds are derived from recombinant bacteriophage or phagemid vector. The antisense compds. were specific and effective for the elimination of target mRNA. Thus, the system of the present invention is used as temporary knock-down system to unveil functions of genes crit. for diseases. The system of the present invention can be adopted not only for functional genomics but also for effectively validating target for antisense or other mol. therapeutics against various malignancies, infections, and other diseases by blocking specific genes involved in the disease.

REFERENCE COUNT: 13 THERE ARE 13 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L20 ANSWER 3 OF 3 CA COPYRIGHT 2003 ACS
ACCESSION NUMBER: 137:227643 CA
TITLE: Large **circular** target-specific **antisense** nucleic acids for inhibition of gene expression and therapy
INVENTOR(S): Park, Jong-gu; Huh, Bin
PATENT ASSIGNEE(S): Welgene Inc., S. Korea
SOURCE: Eur. Pat. Appl., 38 pp.
CODEN: EPXXDW
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
EP 1239034	A2	20020911	EP 2002-4933	20020305
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR				
US 2002182181	A1	20021205	US 2002-66498	20020130
AU 2002018831	A5	20020912	AU 2002-18831	20020228
CN 1374316	A	20021016	CN 2002-107110	20020308
US 2002168631	A1	20021114	US 2002-94183	20020308

PRIORITY APPLN. INFO.: KR 2001-12061 A 20010308
WO 2001-KR1730 A 20011013

AB The present application describes a large **circular** target-specific **antisense** mol. that is effective in ablating RNA and protein expression. The large **circular antisense** mol. is used to treat any human disease in which modulation of gene expression can be beneficial to intervene in the disease initiation and progression. Thus, large circular nucleic acid mols. were constructed employing a phagemid vector and the M13KO7 helper bacteriophages contg. the antisense sequence for TNF-.alpha., NF-.kappa.B, c-myc, c-myb, c-Ki-ras, and cdk2. TNF.alpha.-M13AS was tested for its circular structure and stability to nucleases. The antisense mols. specifically reduced expression of their resp. mRNA, and inhibited growth of cancer cells.

=> s park, J?/au; s Moon, I?/au
L21 35781 PARK, J?/AU

L22 800 MOON, I?/AU

=> s (l21 or l22) and m13
L23 8 (L21 OR L22) AND M13

```
=> dup rem l23
PROCESSING COMPLETED FOR L23
L24           5 DUP REM L23 (3 DUPLICATES REMOVED)

=> d his

     (FILE 'HOME' ENTERED AT 13:02:29 ON 26 MAY 2003)

     FILE 'MEDLINE, BIOSIS, EMBASE, CA, SCISEARCH' ENTERED AT 13:02:49 ON 26
     MAY 2003
L1        101549 S ANTISENSE OR (COMPLE (2N) (OLIGO? OR NUCLEI?))
L2        217407 S ANTISENSE? OR (COMPLE? (2N) (OLIGO? OR NUCLE?))
L3         77824 S SSDNA OR (SINGL? STRAND? (2N) (DNA OR RNA OR (NUCLE? ACID?)))
L4          4019 S L2 AND L3
L5           603 S L2 (5N) L3
L6           474 S L2 (3N) L3
L7            26 S L6 AND M13
L8            15 DUP REM L7 (11 DUPLICATES REMOVED)
L9        123487 S ANTISENSE? OR (COMPLEM? (2N) (OLIGO? OR NUCLE?))
L10       126636 S ANTISENSE? OR (ANTI (N) SENSE) OR (COMPLEM? (2N) (OLIGO? OR N
L11          231 S L10 AND M13
L12            1 S L10 (2N) M 13
L13            9 S L10 (2N) M13
L14            6 DUP REM L13 (3 DUPLICATES REMOVED)
L15         2854 S L3 AND M13
L16           69 S L15 AND L10
L17            1 S L16 AND (CIRC? (5N) L10)
L18          186 S (CIRC? (5N) L10)
L19            3 S L18 AND M13
L20            3 DUP REM L19 (0 DUPLICATES REMOVED)
L21        35781 S PARK, J?/AU
L22          800 S MOON, I?/AU
L23            8 S (L21 OR L22) AND M13
L24            5 DUP REM L23 (3 DUPLICATES REMOVED)

=> s l24 and l10
L25           5 L24 AND L10

=> d l25 ibib abs 1-5

L25  ANSWER 1 OF 5     MEDLINE
ACCESSION NUMBER:    91332994     MEDLINE
DOCUMENT NUMBER:     91332994   PubMed ID: 1714513
TITLE:               Deletions in the tRNA(Lys) primer-binding site of human
                     immunodeficiency virus type 1 identify essential regions
                     for reverse transcription.
AUTHOR:              Rhim H; Park J; Morrow C D
CORPORATE SOURCE:    Department of Microbiology, University of Alabama,
                     Birmingham 35294.
CONTRACT NUMBER:     AI-27767 (NIAID)
     AI27290 (NIAID)
SOURCE:              JOURNAL OF VIROLOGY, (1991 Sep) 65 (9) 4555-64.
                     Journal code: 0113724. ISSN: 0022-538X.
PUB. COUNTRY:        United States
DOCUMENT TYPE:       Journal; Article; (JOURNAL ARTICLE)
LANGUAGE:            English
FILE SEGMENT:        Priority Journals; AIDS
ENTRY MONTH:         199109
ENTRY DATE:          Entered STN: 19911006
                     Last Updated on STN: 19970203
                     Entered Medline: 19910919
AB   The initiation of human immunodeficiency virus type 1 (HIV-1) reverse
```

transcription occurs by the extension of a tRNA primer bound near the 5' end of the genomic RNA at a position termed the primer-binding site (PBS). The PBS is an 18-nucleotide region of the HIV-1 genome complementary to cellular tRNA(Lys). To further investigate the sequence requirements for the PBS in reverse transcription, deletions in the PBS were created and subcloned into a plasmid containing the infectious HIV-1 proviral genome. The mutations deleted the entire PBS (delta PBS) or the first 9 (delta 1-9), the second 9 (delta 10-18), or 12 (delta 7-18) nucleotides of the PBS. An additional mutation in the PBS was created in which the second nine nucleotides were deleted and nine additional nucleotides were substituted [Lys(1-9)]. The transfection of plasmids containing the wild-type or mutant proviral genomes into tissue culture cells resulted in expression of the HIV-1 gag and env gene products, as determined by immunoprecipitation using sera from AIDS patients. HIV-1 virus was released from the transfected cells, as determined by analysis of the supernatants for reverse transcriptase activity. The infectivity of the viruses derived from the transfection was examined by coculture experiments with SupT1 cells, which support high-level replication of HIV-1. The transfection of plasmids containing HIV-1 proviral genomes with the delta PBS and PBS (delta 1-9) mutations did not produce infectious virus. In contrast, the HIV-1 proviral genomes with the delta 10-18, delta 7-18, and Lys(1-9) mutations in the PBS produced infectious virus upon transfection, although the kinetics of appearance was significantly delayed for the mutant viruses compared with the wild type. To further explore the nature of this defect, the PBS region from integrated proviral genomes was amplified by polymerase chain reaction and individual DNA products were subcloned into M13mp19, followed by a sequence analysis of the PBS region from individual **M13** phage clones. In each of the PBS regions examined, the 18-**nucleotide** PBS **complementary** to tRNA(Lys) was present. However, nucleotide deletions and insertions were found 3' to the PBS from the samples derived from the transfection of plasmids containing mutant proviral genomes. Upon reinfection, the revertant viruses maintained the deletions 3' to the PBS and had kinetics of replication similar to that of the wild-type virus.(ABSTRACT TRUNCATED AT 400 WORDS)

L25 ANSWER 2 OF 5 CA COPYRIGHT 2003 ACS
ACCESSION NUMBER: 137:380940 CA
TITLE: Unigene unidirectional **antisense** library derived from recombinant bacteriophage or phagemid vector for therapy and massive functional genomics
INVENTOR(S): **Park, Jong-Gu; Moon, Ik-Jae;** Lee, Yun-Han
PATENT ASSIGNEE(S): Welgene Pharmaceuticals, Inc., S. Korea
SOURCE: PCT Int. Appl., 79 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 2
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2002092807	A1	20021121	WO 2002-IB1753	20020516

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, CH,

CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR,
BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG
PRIORITY APPLN. INFO.: KR 2001-27071 A 20010517
AB The present invention provides a high throughput system for functional genomics using a unigene **antisense** library comprising large circular (LC)-**antisense** compds. The said large circular (LC)-**antisense** compds are derived from recombinant bacteriophage or phagemid vector. The **antisense** compds. were specific and effective for the elimination of target mRNA. Thus, the system of the present invention is used as temporary knock-down system to unveil functions of genes crit. for diseases. The system of the present invention can be adopted not only for functional genomics but also for effectively validating target for **antisense** or other mol. therapeutics against various malignancies, infections, and other diseases by blocking specific genes involved in the disease.
REFERENCE COUNT: 13 THERE ARE 13 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L25 ANSWER 3 OF 5 CA COPYRIGHT 2003 ACS
ACCESSION NUMBER: 137:364368 CA
TITLE: Libraries of RNAs that can be prepared as large circular molecules and their use in high throughput screening and functional genomics
INVENTOR(S): **Park, Jong-Gu; Moon, Ik-Jae;** Lee, Yun-Han
PATENT ASSIGNEE(S): Welgene, Inc., S. Korea
SOURCE: PCT Int. Appl., 87 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 2
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2002092808	A1	20021121	WO 2002-IB735	20020309

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG
PRIORITY APPLN. INFO.: KR 2001-27071 A 20010517
AB The present invention provides a high-throughput system for functional genomics using a random gene unidirectional **antisense** library comprising large circular RNAs including on or more an **antisense** segments. The **antisense** RNAs are specific and effective inhibitors of translation of a target mRNA. Thus, the system may be effectively used as temporary knock-down system to unveil functions of genes crit. for diseases. The RNA sequences are obtained from a specific biol. state, such as a disease state, by methods such as subtractive hybridization. The selected sequences may then be used to selectively inhibit state-specific genes. These large sequences are generated from bacteriophage or phagemid clones and because they may be several hundred or thousand base pairs long, they are accurate and specific in their effects. Use of bacteriophage **M13** and phagemids to generate large circular RNAs inhibiting expression of genes for tumor necrosis factor .alpha. and NF-.kappa.B is demonstrated. The system of the present

invention can be adapted not only for functional genomics but also for effectively validating target for **antisense** or other mol. therapeutics against various malignancies, infections, and other diseases by blocking specific genes involved in the disease.

REFERENCE COUNT: 9 THERE ARE 9 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L25 ANSWER 4 OF 5 CA COPYRIGHT 2003 ACS
ACCESSION NUMBER: 137:227643 CA
TITLE: Large circular target-specific **antisense** nucleic acids for inhibition of gene expression and therapy
INVENTOR(S): **Park, Jong-gu**; Huh, Bin
PATENT ASSIGNEE(S): Welgene Inc., S. Korea
SOURCE: Eur. Pat. Appl., 38 pp.
CODEN: EPXXDW
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
EP 1239034	A2	20020911	EP 2002-4933	20020305
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR				
US 2002182181	A1	20021205	US 2002-66498	20020130
AU 2002018831	A5	20020912	AU 2002-18831	20020228
CN 1374316	A	20021016	CN 2002-107110	20020308
US 2002168631	A1	20021114	US 2002-94183	20020308

PRIORITY APPLN. INFO.: KR 2001-12061 A 20010308
WO 2001-KR1730 A 20011013

AB The present application describes a large circular target-specific **antisense** mol. that is effective in ablating RNA and protein expression. The large circular **antisense** mol. is used to treat any human disease in which modulation of gene expression can be beneficial to intervene in the disease initiation and progression. Thus, large circular nucleic acid mols. were constructed employing a phagemid vector and the M13KO7 helper bacteriophages contg. the **antisense** sequence for TNF-.alpha., NF-.kappa.B, c-myc, c-myb, c-Ki-ras, and cdk2. TNF.alpha.-M13AS was tested for its circular structure and stability to nucleases. The **antisense** mols. specifically reduced expression of their resp. mRNA, and inhibited growth of cancer cells.

L25 ANSWER 5 OF 5 SCISEARCH COPYRIGHT 2003 THOMSON ISI
ACCESSION NUMBER: 91:465703 SCISEARCH
THE GENUINE ARTICLE: GB018
TITLE: DELETIONS IN THE TRANSFER-RNALYS PRIMER-BINDING SITE OF HUMAN-IMMUNODEFICIENCY-VIRUS TYPE-1 IDENTIFY ESSENTIAL REGIONS FOR REVERSE TRANSCRIPTION
AUTHOR: RHIM H; **PARK J**; MORROW C D (Reprint)
CORPORATE SOURCE: UNIV ALABAMA, DEPT MICROBIOL, BIRMINGHAM, AL, 35294
COUNTRY OF AUTHOR: USA
SOURCE: JOURNAL OF VIROLOGY, (1991) Vol. 65, No. 9, pp. 4555-4564.
DOCUMENT TYPE: Article; Journal
FILE SEGMENT: LIFE
LANGUAGE: ENGLISH
REFERENCE COUNT: 38

ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

AB The initiation of human immunodeficiency virus type 1 (HIV-1) reverse transcription occurs by the extension of a tRNA primer bound near the 5' end of the genomic RNA at a position termed the primer-binding site (PBS).

The PBS is an 18-nucleotide region of the HIV-1 genome complementary to cellular tRNA(Lys). To further investigate the sequence requirements for the PBS in reverse transcription, deletions in the PBS were created and subcloned into a plasmid containing the infectious HIV-1 proviral genome. The mutations deleted the entire PBS (DELTA-PBS) or the first 9 (DELTA-1-9), the second 9 (DELTA-10-18), or 12 (DELTA-7-18) nucleotides of the PBS. An additional mutation in the PBS was created in which the second nine nucleotides were deleted and nine additional nucleotides were substituted [Lys(1-9)]. The transfection of plasmids containing the wild-type or mutant proviral genomes into tissue culture cells resulted in expression of the HIV-1 gag and env gene products, as determined by immunoprecipitation using sera from AIDS patients. HIV-1 virus was released from the transfected cells, as determined by analysis of the supernatants for reverse transcriptase activity. The infectivity of the viruses derived from the transfection was examined by coculture experiments with SupT1 cells, which support high-level replication of HIV-1. The transfection of plasmids containing HIV-1 proviral genomes with the DELTA-PBS and PBS (DELTA-1-9) mutations did not produce infectious virus. In contrast, the HIV-1 proviral genomes with the DELTA-10-18, DELTA-7-18, and Lys(1-9) mutations in the PBS produced infectious virus upon transfection, although the kinetics of appearance was significantly delayed for the mutant viruses compared with the wild type. To further explore the nature of this defect, the PBS region from integrated proviral genomes was amplified by polymerase chain reaction and individual DNA products were subcloned into M13mp19, followed by a sequence analysis of the PBS region from individual **M13** phage clones. In each of the PBS regions examined, the 18-**nucleotide** PBS **complementary** to tRNA(Lys) was present. However, nucleotide deletions and insertions were found 3' to the PBS from the samples derived from the transfection of plasmids containing mutant proviral genomes. Upon reinfection, the revertant viruses maintained the deletions 3' to the PBS and had kinetics of replication similar to that of the wild-type virus. These results demonstrate a minimum requirement for the PBS sequence as well as the important role of cellular tRNA(Lys) in the regeneration of the PBS during HIV-1 reverse transcription.

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     (FILE 'HOME' ENTERED AT 13:02:29 ON 26 MAY 2003)

     FILE 'MEDLINE, BIOSIS, EMBASE, CA, SCISEARCH' ENTERED AT 13:02:49 ON 26
     MAY 2003
L1       101549 S ANTISENSE OR (COMPLE (2N) (OLIGO? OR NUCLEI?))
L2       217407 S ANTISENSE? OR (COMPLE? (2N) (OLIGO? OR NUCLE?))
L3        77824 S SSDNA OR (SINGL? STRAND? (2N) (DNA OR RNA OR (NUCLE? ACID?)))
L4         4019 S L2 AND L3
L5          603 S L2 (5N) L3
L6          474 S L2 (3N) L3
L7           26 S L6 AND M13
L8           15 DUP REM L7 (11 DUPLICATES REMOVED)
L9       123487 S ANTISENSE? OR (COMPLEM? (2N) (OLIGO? OR NUCLE?))
L10      126636 S ANTISENSE? OR (ANTI (N) SENSE) OR (COMPLEM? (2N) (OLIGO? OR N
L11         231 S L10 AND M13
L12           1 S L10 (2N) M 13
L13           9 S L10 (2N) M13
L14           6 DUP REM L13 (3 DUPLICATES REMOVED)
L15        2854 S L3 AND M13
L16          69 S L15 AND L10
L17           1 S L16 AND (CIRC? (5N) L10)
L18         186 S (CIRC? (5N) L10)
L19           3 S L18 AND M13
```

```
L20           3 DUP REM L19 (0 DUPLICATES REMOVED)
L21       35781 S PARK, J?/AU
L22         800 S MOON, I?/AU
L23           8 S (L21 OR L22) AND M13
L24           5 DUP REM L23 (3 DUPLICATES REMOVED)
L25           5 S L24 AND L10

=> s l10 and l3
L26       2131 L10 AND L3

=> s l26 and circ?
L27        209 L26 AND CIRC?

=> dup rem l27
PROCESSING COMPLETED FOR L27
L28         114 DUP REM L27 (95 DUPLICATES REMOVED)

=> sl 28 and py<=2001
SL IS NOT A RECOGNIZED COMMAND
The previous command name entered was not recognized by the system.
For a list of commands available to you in the current file, enter
"HELP COMMANDS" at an arrow prompt (=>).

=> s l28 and py<=2001
   2 FILES SEARCHED...
L29         99 L28 AND PY<=2001

=> s l29 and (l10 (w) circ?)
L30          0 L29 AND (L10 (W) CIRC?)

=> s l29 and (l10 (s) circ?)
L31         28 L29 AND (L10 (S) CIRC?)

=> d l31 1-28 ibib abs

L31  ANSWER 1 OF 28     MEDLINE
ACCESSION NUMBER:   1999115548     MEDLINE
DOCUMENT NUMBER:    99115548   PubMed ID: 9916082
TITLE:              The R-type pyocin of Pseudomonas aeruginosa C is a
                    bacteriophage tail-like particle that contains
                    single-stranded DNA.
AUTHOR:             Lee F K; Dudas K C; Hanson J A; Nelson M B; LoVerde P T;
                    Apicella M A
CORPORATE SOURCE:   Department of Microbiology, College of Medicine, University
                    of Iowa, Iowa City, Iowa, USA.
CONTRACT NUMBER:    AI 18384 (NIAID)
SOURCE:             INFECTION AND IMMUNITY, (1999 Feb) 67 (2) 717-25.
                    Journal code: 0246127. ISSN: 0019-9567.
PUB. COUNTRY:       United States
DOCUMENT TYPE:      Journal; Article; (JOURNAL ARTICLE)
LANGUAGE:           English
FILE SEGMENT:       Priority Journals
OTHER SOURCE:       GENBANK-L06240
ENTRY MONTH:        199903
ENTRY DATE:         Entered STN: 19990324
                    Last Updated on STN: 19990324
                    Entered Medline: 19990309
AB   Pseudomonas aeruginosa R-type pyocin particles have been described as
     bacteriocins that resemble bacteriophage tail-like structures.  Because of
     their unusual structure, we reexamined whether they contained nucleic
     acids.  Our data indicated that pyocin particles isolated from P.
     aeruginosa C (pyocin C) contain DNA.  Probes generated from this DNA by
```

the random-primer extension method hybridized to distinct bands in restriction endonuclease-digested P. aeruginosa C genomic DNA. These probes also hybridized to genomic DNA from 6 of 18 P. aeruginosa strains that produced R-type pyocins. Asymmetric PCR, **complementary oligonucleotide** hybridization, and electron microscopy indicated that pyocin C particles contained closed **circular single -stranded DNA**, approximately 4.0 kb in length. Examination of total intracellular DNA from mitomycin C-induced cultures revealed the presence of two extrachromosomal DNA molecules, a double-stranded molecule and a single-stranded molecule, which hybridized to pyocin DNA. Sequence analysis of 7,480 nucleotides of P. aeruginosa C chromosomal DNA containing the pyocin DNA indicated the presence of pyocin open reading frames with similarities to open reading frames from filamentous phages and cryptic phage elements. We did not observe any similarities to known phage structural proteins or previously characterized pseudomonal prt genes expressing R-type pyocin structural proteins. These studies demonstrate that pyocin particles from P. aeruginosa C are defective phages that contain a novel closed **circular single-stranded DNA** and that this DNA was derived from the chromosome of P. aeruginosa C.

L31 ANSWER 2 OF 28 MEDLINE
ACCESSION NUMBER: 1998440432 MEDLINE
DOCUMENT NUMBER: 98440432 PubMed ID: 9765572
TITLE: Methanococcus jannaschii flap endonuclease: expression, purification, and substrate requirements.
AUTHOR: Rao H G; Rosenfeld A; Wetmur J G
CORPORATE SOURCE: Department of Microbiology, Mount Sinai School of Medicine, New York, New York 10029, USA.
CONTRACT NUMBER: HG01356 (NHGRI)
SOURCE: JOURNAL OF BACTERIOLOGY, **(1998 Oct)** 180 (20) 5406-12.
Journal code: 2985120R. ISSN: 0021-9193.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199810
ENTRY DATE: Entered STN: 19990106
Last Updated on STN: 20000303
Entered Medline: 19981030

AB The flap endonuclease (FEN) of the hyperthermophilic archaeon Methanococcus jannaschii was expressed in Escherichia coli and purified to homogeneity. FEN retained activity after preincubation at 95 degrees C+ for 15 min. A pseudo-Y-shaped substrate was formed by hybridization of two partially **complementary oligonucleotides**. FEN cleaved the strand with the free 5' end adjacent to the single-strand-duplex junction. Deletion of the free 3' end prevented cleavage. Hybridization of a **complementary oligonucleotide** to the free 3' end moved the cleavage site by 1 to 2 nucleotides. Hybridization of excess **complementary oligonucleotide** to the free 5' end failed to block cleavage, although this substrate was refractory to cleavage by the 5'-3' exonuclease activity of Taq DNA polymerase. For verification, the free 5' end was replaced by an internally labeled hairpin structure. This structure was a substrate for FEN but became a substrate for Taq DNA polymerase only after exonucleolytic cleavage had destabilized the hairpin. A **circular** duplex substrate with a 5' single-stranded branch was formed by primer extension of a partially **complementary oligonucleotide** on virion phiX174. This denaturation-resistant substrate was used to examine the effects of temperature and solution properties, such as pH, salt, and divalent ion concentration on the

turnover number of the enzyme.

L31 ANSWER 3 OF 28 MEDLINE
ACCESSION NUMBER: 1998267209 MEDLINE
DOCUMENT NUMBER: 98267209 PubMed ID: 9602151
TITLE: Amplification of target-specific, ligation-depender **circular** probe.
AUTHOR: Zhang D Y; Brandwein M; Hsuih T C; Li H
CORPORATE SOURCE: The Lillian, Henry M. Stratton-Hans Popper Department of Pathology, Department of Otolaryngology, Mount Sinai School of Medicine, New York, NY 10029, USA..
david_zhang@smtplink.mssm.edu
SOURCE: GENE, **(1998 May 12)** 211 (2) 277-85.
Journal code: 7706761. ISSN: 0378-1119.
PUB. COUNTRY: Netherlands
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199807
ENTRY DATE: Entered STN: 19980723
Last Updated on STN: 19980723
Entered Medline: 19980714

AB We describe a novel polymerase chain reaction (PCR)-based gene amplification method utilizing a **circularizable** oligodeoxyribonucleotide probe (C-probe). The C-probe contains two target complementary regions located at each terminus and an interposed generic PCR primer binding region. The hybridization of C-probe to a target brings two termini in direct apposition as the complementary regions of C-probe wind around the target to form a double helix. Subsequent ligation of the two termini results in a covalently linked C-probe that becomes 'locked on to' the target. The **circular** nature of the C-probe allows for the generation of a multimeric **single-stranded DNA** (**ssDNA**) via extension of the **antisense** primer by Taq DNA polymerase along the C-probe and displacement of downstream strand, analogous to 'rolling **circle**' replication of bacteriophage in vivo. This multimeric **ssDNA** then serves as a template for multiple sense primers to hybridize, extend, and displace downstream DNA, generating a large ramified (branching) DNA complex. Subsequent thermocycling denatures the dsDNA and initiates the next round of primer extension and ramification. This model results in significantly improved amplification kinetics (super-exponential) as compared to conventional PCR. Our results show that the C-probe was 1000 times more sensitive than the corresponding linear hemiprobes for detecting Epstein-Barr virus early RNA. The C-probe not only increases the power of amplification but also offers a means for decontaminating carryover amplicons. As the ligated C-probes possess no free termini, they are resistant to exonuclease digestion, whereas contaminated linear amplicons are susceptible to digestion. Treatment of the ligation reaction mixture with exonuclease prior to amplification eliminated the amplicon contaminant, which could also have been co-amplified with the same PCR primers; only the ligated C-probes were amplified. The combined advantages of the C-probe and thermocycling have a broad applicability for the detection of both DNA and RNA. Finally, we described a novel isothermal amplification method, ramification extension amplification, utilizing **circular** nature of C-probe and displacement activity of DNA polymerase.

L31 ANSWER 4 OF 28 MEDLINE
ACCESSION NUMBER: 1998167937 MEDLINE
DOCUMENT NUMBER: 98167937 PubMed ID: 9500923
TITLE: The beta protein of phage lambda promotes strand exchange.
AUTHOR: Li Z; Karakousis G; Chiu S K; Reddy G; Radding C M

CORPORATE SOURCE: Department of Genetics, Yale University School of Medicine, New Haven, CT 06510, USA.
CONTRACT NUMBER: PO1 CA39238 (NCI)
R37 GM33504 (NIGMS)
SOURCE: JOURNAL OF MOLECULAR BIOLOGY, **(1998 Mar 6)** 276 (4) 733-44.
Journal code: 2985088R. ISSN: 0022-2836.
PUB. COUNTRY: ENGLAND: United Kingdom
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199805
ENTRY DATE: Entered STN: 19980514
Last Updated on STN: 20000303
Entered Medline: 19980504

AB Bacteriophage lambda encodes a 28 kDa protein called beta that binds to **single-stranded DNA** and promotes the renaturation of complementary single strands. beta Protein fails to bind directly to duplex DNA but remains bound to the DNA product of renaturation that beta itself catalyzes. These observations led to an examination of the ability of beta protein to promote strand exchange. beta Protein caused the replacement of a 43-mer oligonucleotide annealed to M13 **circular single-stranded DNA** by a homologous 63-mer whose 20 extra **nucleotide** residues were **complementary** to the adjacent 3' region of M13 DNA. The role of beta protein in this reaction was manifested in several ways: beta protein pushed the exchange through four to eight mismatches, which blocked exchange mediated by spontaneous renaturation and branch migration; beta imposed a polarity on the strand exchange that was lacking in the spontaneous reaction; and beta remained bound to the heteroduplex product of strand exchange. These observations reveal a mechanism by which a protein can drive strand exchange in one direction without using ATP or any other exogenous source of energy.

L31 ANSWER 5 OF 28 MEDLINE
ACCESSION NUMBER: 1998060892 MEDLINE
DOCUMENT NUMBER: 98060892 PubMed ID: 9396802
TITLE: Inhibitory properties of double-helix-forming **circular** oligonucleotides.
AUTHOR: Azhayeva E; Azhayev A; Auriola S; Tengvall U; Urtti A; Lonnberg
CORPORATE SOURCE: Department of Pharmaceutical Chemistry, University of Kuopio, FIN-70211 Kuopio, Finland.
SOURCE: NUCLEIC ACIDS RESEARCH, **(1997 Dec 15)** 25 (24) 4954-61.
Journal code: 0411011. ISSN: 0305-1048.
PUB. COUNTRY: ENGLAND: United Kingdom
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199802
ENTRY DATE: Entered STN: 19980306
Last Updated on STN: 19980306
Entered Medline: 19980224

AB Several **circular** oligonucleotides were synthesized and characterized by electrospray ionization mass spectrometry. Experiments on termination of primer extension catalysed by DNA polymerases, Klenow fragment and Tth have demonstrated that a double helix forming **circular** 2'-deoxyribooligomer containing a 25mer sequence complementary to the target **single-stranded DNA** along with a 34mer random mismatching stretch appears to be a

potent inhibitor of replication in vitro. Studies on inhibition of luciferase gene expression in a cell-free transcription-translation system have shown that a duplex forming **circular** 2'-deoxyribooligonucleotide containing a 25mer sequence complementary to the target mRNA and a 14mer random mismatching stretch can serve as an effective **antisense** compound as a standard linear **complementary oligomer**. Features of double helix forming **circular** oligonucleotides composed of 2'-deoxyribonucleosides seem to be useful for the design of new antigene and **antisense** agents.

L31 ANSWER 6 OF 28 MEDLINE
ACCESSION NUMBER: 94252981 MEDLINE
DOCUMENT NUMBER: 94252981 PubMed ID: 8195068
TITLE: Characterization of a region of plasmid pBL1 of Brevibacterium lactofermentum involved in replication via the rolling **circle** model.
AUTHOR: Fernandez-Gonzalez C; Cadenas R F; Noirot-Gros M F; Martin J F; Gil J A
CORPORATE SOURCE: Section of Microbiology, Faculty of Biology, University of Leon, Spain.
SOURCE: JOURNAL OF BACTERIOLOGY, **(1994 Jun)** 176 (11) 3154-61.
Journal code: 2985120R. ISSN: 0021-9193.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199406
ENTRY DATE: Entered STN: 19940707
Last Updated on STN: 19940707
Entered Medline: 19940630

AB The minimal region for autonomous replication of pBL1, a 4.5-kb cryptic plasmid of Brevibacterium lactofermentum ATCC 13869 that has been used to construct a variety of corynebacterium vectors, was shown to be contained on a 1.8-kb HindII-SphI DNA fragment. This region contains two open reading frames (ORFs) (ORF1 and ORF5) which are essential for pBL1 replication in B. lactofermentum. Accumulation of single-strand intermediates in some of the constructions indicates that plasmid pBL1 replicates via the rolling **circle** replication model; its plus strand and minus strand were identified by hybridization with two synthetic **oligonucleotide** probes **complementary** to each pBL1 strand. ORF1 seems to encode the Rep protein and showed partial homology with sequences for Rep proteins from Streptomyces plasmids which replicate via rolling **circle** replication such as pIJ101, pSB24, and pJV1.

L31 ANSWER 7 OF 28 MEDLINE
ACCESSION NUMBER: 89301133 MEDLINE
DOCUMENT NUMBER: 89301133 PubMed ID: 2662813
TITLE: Oligodeoxynucleotide-directed cleavage and repair of a single-stranded vector: a method of site-specific mutagenesis.
AUTHOR: Zhu D L
CORPORATE SOURCE: Institut Jacques Monod, CNRS, Paris, France.
SOURCE: ANALYTICAL BIOCHEMISTRY, **(1989 Feb 15)** 177 (1) 120-4.
Journal code: 0370535. ISSN: 0003-2697.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals

ENTRY MONTH: 198908
ENTRY DATE: Entered STN: 19900309
Last Updated on STN: 19900309
Entered Medline: 19890810

AB A simple and efficient site-specific mutagenesis method is described. First, a single-stranded (ss) **circular** vector is linearized at the site where the desired mutation will be introduced. To do this, an **oligodeoxynucleotide complementary** to the target region of the ss vector and containing a restriction enzyme recognition sequence is annealed to the **circular** ss vector, and the partial double-strand formed is subsequently cleaved with that enzyme. Then, another oligodeoxynucleotide spanning the nick and carrying the mutation is annealed to the linearized ss DNA template and the annealed mixture is used directly to transform Escherichia coli without prior enzymatic DNA synthesis in vitro. The procedure has been applied successfully to constructing insertion, deletion, and point mutations in both M13 phage vectors and plasmid vectors containing the f1 origin of replication.

L31 ANSWER 8 OF 28 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 1995:341946 BIOSIS
DOCUMENT NUMBER: PREV199598356246
TITLE: Properties and anti-HIV activity of **circular** sense and **antisense** oligonucleotides.
AUTHOR(S): Yamakawa, Hidefumi; Ishibashi, Toshiaki; Nakashima, Hideki; Yamamoto, Naoki; Takai, Kazuyuki; Takaku, Hiroshi (1)
CORPORATE SOURCE: (1) Rational Drug Design Lab., Misato, Matsukawa, Fukushima, Fukushima 960-12 Japan
SOURCE: Nucleosides & Nucleotides, (1995) Vol. 14, No. 3-5, pp. 1149-1152.
ISSN: 0732-8311.
DOCUMENT TYPE: Article
LANGUAGE: English

AB The **circularization** of a 48 mer oligonucleotide was investigated by using enzymatic ligation with T4 DNA ligase. This method yielded 30% **circular** molecules. The **circular** oligonucleotides are molecules with no free ends and are therefore more resistant to exonuclease attack. The **circular** oligonucleotide has remarkably increased Tm values as compared to the nicked and double stranded DNAs. However, the RNase H activity is lower than that with a **single stranded DNA**. We also describe the anti-HIV activity of a **circular** oligonucleotide.

L31 ANSWER 9 OF 28 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 1994:251391 BIOSIS
DOCUMENT NUMBER: PREV199497264391
TITLE: Base pairing and steric interactions between pyrimidine strand bridging loops and the purine strand in DNA pyrimidine-purine-pyrimidine triplexes.
AUTHOR(S): Booher, Mark A.; Wang, Shaohui; Kool, Eric T. (1)
CORPORATE SOURCE: (1) Dep. Chem., Univ. Rochester, Rochester, NY 14627 USA
SOURCE: Biochemistry, (1994) Vol. 33, No. 15, pp. 4645-4651.
ISSN: 0006-2960.
DOCUMENT TYPE: Article
LANGUAGE: English

AB Bimolecular triple-helical DNA complexes recently have found use in a new strategy for the recognition of **single-stranded nucleic acids**, in which **circular** (Kool, 1991; Prakash & Kool, 1992) or hairpin-shaped (Giovannangeli et al., 1991; D'Souza & Kool, 1992) oligonucleotides bind these single strands by triplex formation. Bimolecular triplexes may also be formed in vivo as H-DNA, where this structure may potentially play a role in gene expression and recombination (Belotserkovskii et al., 1990; Hanvey et al., 1989;

Shimizu et al., 1989). In all of these complexes, the central strand of the triplex must pass beyond the loop that bridges the outer two strands, and models and preliminary experiments have indicated that there may be important interactions between this central strand and the loop (Prakash & Kool, 1992). We now report thermal denaturation studies carried out specifically to investigate these interactions in detail, using as a model the 5'-loop and 3'-loop complexes formed between 14 pyrimidine oligodeoxynucleotides having the sequence 5'-dTTCTTTTCL-1TTTL-5CTTTTCTT, where L-1 and L-5 represent varied nucleotides in the loop (which is underlined), and eight target strands having the sequence 5'-dCCCCCFAAGAAAAG-3' or 5'-dGAAAAGAAFCCCCC-3', where F is a varied nucleotide flanking the triplex in the central strand. Results correlated from 64 different sequence combinations show that there is wide variation in the stabilities of the complexes, indicating specific and substantial interactions between the nucleotides at the L-1, F, and L-5 positions. Melting temperatures at pH 7.0 range from 17.0 degree C to 34.6 degree C and free energies (37 degree C) range from -3.2 to -7.8 kcal mol-1. Several general conclusions are drawn from the 64 combinations studied: (1) Extra stability is gained when one of the first (L-1) or fifth (L-5) nucleotides in the loop is complementary to the F nucleotide in the purine strand, with an average advantage of 1.9-3.0 degree C in T-m and 0.6 kcal in free energy. (2) Even higher stability is gained when both the L-1 and L-5 **nucleotides** are **complementary** to the flanking F nucleotide. The advantage (relative to no complementarily) is 3.2-4.7 degree C in T-m and 1.1-1.5 kcal in free energy, on average; however, evidence indicates that this interaction is not the result of standard triple-helix pairing. (3) The correct choice of loop nucleotides can add both binding affinity and sequence selectivity to bimolecular triplexes. Binding studies of two **circular** oligodeoxynucleotides constructed as a test of the loop studies shows that the results allow semiquantitative predictions of the stabilities of bimolecular triplexes that involve these loop interactions. In the design of synthetic oligonucleotides as triplex-forming agents, the results suggest optimal choices of loop nucleotides for binding a given target sequence. The results may also aid in the understanding of the relative stabilities of H-DNA complexes.

L31 ANSWER 10 OF 28 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 1993:432235 BIOSIS
DOCUMENT NUMBER: PREV199396086860
TITLE: Analysis of replication of HIV-1 by mutagenesis of reverse transcriptase and nucleocapsid protein.
AUTHOR(S): Moelling, Karein (1); Volkmann, Silke (1); Dannull, Jens (1); Surovoy, Andrej; Jung, Gunter
CORPORATE SOURCE: (1) Max-Planck-Inst. Molekulare Genetik, Abt. Schuster, Ihnestrasse 73, W-1000 Berlin 33 Germany
SOURCE: AIDS-Forschung, (1993) Vol. 8, No. 5, pp. 243-248. ISSN: 0179-3098.
DOCUMENT TYPE: Article
LANGUAGE: English
SUMMARY LANGUAGE: English; German
AB Replication of retroviral RNA into double-stranded DNA involves RNA-dependent, DNA-dependent DNA synthesis by reverse transcriptase (RT) and hydrolysis of RNA-DNA hybrids by action of the RNase H. Both enzyme activities are coupled and cooperate. Among all 14 known RT sequences 7 amino acids are highly conserved in the RNase H domain. Three of these have been mutagenized and their properties studied in vitro, aminoacid residue glutamine 475 to glutamate (Q475E), asparagine 495 to aspartate and histidine 539 to glutamine (H539N). One of the mutants does not recognize the polypurine tract, PPT, the primer for plus-strand DNA synthesis, a defect which makes this mutant noninfectious. Based on this observation, the PPT is under investigation as target for **anti-**

sense or triple helix forming (TFO) DNA oligonucleotides in order to prevent retroviral replication. Furthermore, the nucleocapsid protein p7 (NCp7) protein has been analyzed. It binds to **single-stranded** (ss) **RNA**, **ssDNA** and double-stranded (ds) DNA in vitro. Modification of its zinc-finger structures affects binding to **ssDNA** but not to RNA and dsDNA. The NCp7 causes a slight stimulation of RNA-dependent DNA-synthesis by the RT in vitro. Furthermore, the conformation of NCp7 has been determined by **circular** dichroism (CD).

L31 ANSWER 11 OF 28 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 1980:159341 BIOSIS
DOCUMENT NUMBER: BA69:34337
TITLE: HEPATITIS B VIRAL DNA MOLECULES HAVE COHESIVE ENDS.
AUTHOR(S): SATTLER F; ROBINSON W S
CORPORATE SOURCE: DEP. MED., STANFORD UNIV. SCH. MED., STANFORD, CALIF. 94305, USA.
SOURCE: J VIROL, (1979) 32 (1), 226-232.
CODEN: JOVIAM. ISSN: 0022-538X.
FILE SEGMENT: BA; OLD
LANGUAGE: English

AB Hepatitis B virus DNA made fully double stranded by a virion DNA polymerase reaction could be converted from **circular** to linear molecules by heating in 10 mM NaCl at 77.degree. C or in 100 mM NaCl at 90.degree. C for 15 min. Heat-generated linear hepatitis B virus DNA was reannealed to **circular** molecules by incubating in higher salt concentrations. The identity of the molecular forms was established by their electrophoretic mobility and appearance in electron micrographs. Recircularization was blocked by reacting linear molecules with nuclease S1 or avian myeloblastosis virus reverse transcriptase. The heated linear **DNA** apparently had **single-stranded** ends with **complementary nucleotide** sequences. A discontinuity or nick is present in each strand of the **circular** DNA molecule after the single-stranded region is made double stranded by the virion DNA polymerase reaction is suggested. The difference in contour length by EM of **circular** and linear molecules spread under aqueous conditions suggested that the discontinuities in the two strands were about 270 base pairs apart. The amount of nucleotide incorporated into the ends of heat-generated linear hepatitis B virus DNA by reverse transcriptase suggested that the single-stranded ends were about 305 bases in length. This fully double-stranded linear DNA was cleaved with EcoRI or HpaI restriction endonuclease. The sum of the 2 fragments generated by each totaled 3510 base pairs, 310 base pairs greater than the contour length of **circular** hepatitis B virus DNA which represents a 3rd estimate of the distance between the discontinuities in the 2 DNA strands of **circular** DNA. Restriction endonuclease cleavage also indicated that the ends of heated linear DNA which correspond to the discontinuities in the 2 strands of the **circular** DNA are at unique sites in the DNA with respect to the restriction sites.

L31 ANSWER 12 OF 28 EMBASE COPYRIGHT 2003 ELSEVIER SCI. B.V.
ACCESSION NUMBER: 2001396404 EMBASE
TITLE: Effect of secondary structure on the thermodynamics and kinetics of PNA hybridization to DNA hairpins.
AUTHOR: Kushon S.A.; Jordan J.P.; Seifert J.L.; Nielsen H.; Nielsen P.E.; Armitage B.A.
CORPORATE SOURCE: B.A. Armitage, Department of Chemistry, Carnegie Mellon University, 4400 Fifth Avenue, Pittsburgh, PA 15213-3890, United States. army@cyrus.andrew.cmu.edu
SOURCE: Journal of the American Chemical Society, (7 Nov 2001) 123/44 (10805-10813).
Refs: 89

ISSN: 0002-7863 CODEN: JACSAT
COUNTRY: United States
DOCUMENT TYPE: Journal; Article
FILE SEGMENT: 029 Clinical Biochemistry
LANGUAGE: English
SUMMARY LANGUAGE: English
AB The binding of a series of PNA and DNA probes to a group of unusually stable DNA hairpins of the tetraloop motif has been observed using absorbance hypochromicity (ABS), **circular** dichroism (CD), and a colorimetric assay for PNA/DNA duplex detection. These results indicate that both stable PNA-DNA and DNA-DNA duplexes can be formed with these target hairpins, even when the melting temperatures for the resulting duplexes are up to 50.degree.C lower than that of the hairpin target. Both hairpin/single-stranded and hairpin/hairpin interactions are considered in the scope of these studies. Secondary structures in both target and probe molecules are shown to depress the melting temperatures and free energies of the probe-target duplexes. Kinetic analysis of hybridization yields reaction rates that are up to 160-fold slower than hybridization between two unstructured strands. The thermodynamic and kinetic obstacles to hybridization imposed by both target and probe secondary structure are significant concerns for the continued development of **antisense** agents and especially diagnostic probes.

L31 ANSWER 13 OF 28 EMBASE COPYRIGHT 2003 ELSEVIER SCI. B.V.
ACCESSION NUMBER: 2000379382 EMBASE
TITLE: Peptide nucleic acids: Versatile tools for gene therapy strategies.
AUTHOR: Dean D.A.
CORPORATE SOURCE: D.A. Dean, Div. Pulmonary/Critical Care Med., Northwestern University, Medical School, 300 E. Superior Ave., Chicago, IL 60611, United States. dean@northwestern.edu
SOURCE: Advanced Drug Delivery Reviews, (15 Nov 2000) 44/2-3 (81-95).
Refs: 72
ISSN: 0169-409X CODEN: ADDREP
PUBLISHER IDENT.: S 0169-409X(00)00087-9
COUNTRY: Netherlands
DOCUMENT TYPE: Journal; General Review
FILE SEGMENT: 022 Human Genetics
029 Clinical Biochemistry
030 Pharmacology
037 Drug Literature Index
039 Pharmacy
LANGUAGE: English
SUMMARY LANGUAGE: English
AB Peptide nucleic acids, or PNAs, are oligonucleotide analogs in which the phosphodiester backbone is replaced with a polyamide structure. First synthesized less than 10 years ago, they have received great attention due to their several favorable properties, including resistance to nuclease and protease digestion, stability in serum and cell extracts, and their high affinity for RNA and single and double-stranded DNA targets. Although initially designed and demonstrated to function as **antisense** and antigene reagents that inhibit both transcription and translation by steric hindrance, more recent applications have included gene activation by synthetic promoter formation and mutagenesis of chromosomal targets. Most notably for gene delivery, they have been used to specifically label plasmids and act as adapters to link synthetic peptides or ligands to the DNA. Thus, their great potential lies in the ability to attach specific targeting peptides to plasmids to **circumvent** such barriers to gene transfer as cell-targeting or nuclear localization, thereby increasing the efficacy of gene therapy. Copyright (C) 2000 Elsevier Science B.V.

L31 ANSWER 14 OF 28 EMBASE COPYRIGHT 2003 ELSEVIER SCI. B.V.
ACCESSION NUMBER: 94258880 EMBASE
DOCUMENT NUMBER: 1994258880
TITLE: Strand displacement amplification as an in vitro model for rolling-**circle** replication: Deletion formation and evolution during serial transfer.
AUTHOR: Walter N.G.; Strunk G.
CORPORATE SOURCE: Department of Biochemical Kinetics, Max Planck Biophysical Chem. Inst., Am Fassberg 11,D-37077 Gottingen, Germany
SOURCE: Proceedings of the National Academy of Sciences of the United States of America, (1994) 91/17 (7937-7941). ISSN: 0027-8424 CODEN: PNASA6
COUNTRY: United States
DOCUMENT TYPE: Journal; Article
FILE SEGMENT: 029 Clinical Biochemistry
LANGUAGE: English
SUMMARY LANGUAGE: English

AB Strand displacement amplification is an isothermal DNA amplification reaction based on a restriction endonuclease nicking its recognition site and a polymerase extending the nick at its 3' end, displacing the downstream strand. The reaction resembles rolling-**circle** replication of single-stranded phages and small plasmids. The displaced sense strand serves as target for an **antisense** reaction and vice versa, resulting in exponential growth and the autocatalytic nature of this in vitro reaction as long as the template is the limiting agent. We describe the optimization of strand displacement amplification for in vitro evolution experiments under serial transfer conditions. The reaction was followed and controlled by use of the fluorescent dye thiazole orange binding to the amplified DNA. We were able to maintain exponential growth conditions with a doubling time of 3.0 min throughout 100 transfers or .simeq.350 molecular generations by using an automatic handling device. Homology of in vitro amplification with rolling-**circle** replication was mirrored by the occurring evolutionary processes. Deletion events most likely caused by a slipped mispairing mechanism as postulated for in vivo replication took place. Under our conditions, the mutation rate was high and a molecular quasi-species formed with a mutant lacking internal hairpin formation ability and thus outgrowing all other species under dGTP/dCTP deficiency.

L31 ANSWER 15 OF 28 CA COPYRIGHT 2003 ACS
ACCESSION NUMBER: 135:29817 CA
TITLE: Generation of **single-strand circular DNA** from two or more hairpin **oligonucleotides** with **complementary** single-strand ends
INVENTOR(S): Abarzua, Patricio
PATENT ASSIGNEE(S): Molecular Staging Inc., USA
SOURCE: PCT Int. Appl., 42 pp. CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2001040516	A2	20010607	WO 2000-US32370	20001128 <--
WO 2001040516	A3	20020711		

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT,

LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU,
SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, UZ, VN, YU,
ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY,
DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF,
BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG

CA 2360342	AA	20010607	CA 2000-2360342	20001128	<--
EP 1238105	A2	20020911	EP 2000-980827	20001128	
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR					
US 6498023	B1	20021224	US 2000-723685	20001128	
PRIORITY APPLN. INFO.:			US 1999-168511P	P 19991202	
			WO 2000-US32370	W 20001128	

AB The present invention provides a method for the rapid simultaneous prodn. of a plurality of **single-stranded DNA circles** having a predetd. size and nucleotide sequence using pre-designed hairpin **oligonucleotides** contg. **complementary** sequences for directing ligation to form dumbbell-shaped monomers followed by heat denaturation to yield **single-stranded DNA circles**.

L31 ANSWER 16 OF 28 CA COPYRIGHT 2003 ACS

ACCESSION NUMBER:	133:248497 CA
TITLE:	Targeting of **single-stranded DNA** and **RNA** containing adjacent pyrimidine and purine tracts by triple helix formation with **circular** and clamp oligonucleotides
AUTHOR(S):	Maksimenko, Andrei V.; Volkov, Evgueny M.; Bertrand, Jean-Remi; Porumb, Horea; Malvy, Claude; Shabarova, Zoe A.; Gottikh, Marina B.
CORPORATE SOURCE:	Belozersky Research Institute of Physico-Chemical Biology and Department of Chemistry, Moscow State University, Russia
SOURCE:	European Journal of Biochemistry (**2000**), 267(12), 3592-3603 CODEN: EJBCAI; ISSN: 0014-2956
PUBLISHER:	Blackwell Science Ltd.
DOCUMENT TYPE:	Journal
LANGUAGE:	English

AB The aim of this work was to construct an anti-messenger targeted to the pim-1 oncogene transcript, based on **circular** or clamp oligodeoxyribonucleotides. The formation of bimol. triplexes by clamp or **circular** oligonucleotides was investigated using single-stranded targets of both DNA (5'-CCCTCCTTTGAAGAA-3') and RNA type (5'-CCCUCCUUUGAAGAA-3'). The third, Hoogsteen strand of the triplex was represented by G,T-rich sequences. The secondary structures of the complexes were detd. by thermal denaturation, CD and gel mobility shift expts. and shown to depend on the nature of the target strand. With DNA as target, the sequence of a clamp (or **circular**) oligonucleotide that formed the triple helix was 3'-GGGAGGAAACTTCTTTT-TTGTTGTTT-TT-GGTGGG-5', where the first TT dinucleotide (in italics) is a linker and the second TT (bold) represents the bridge through which the Hoogsteen strand switches from one strand of the Watson-Crick duplex to the other, once the duplex is formed by the corresponding portion of the anti-messenger (underlined). The portion of the Hoogsteen sequence of the triplex between the two TT dinucleotides binds to the 3' extremity of the target strand and runs parallel to it. The portion situated at the 5' end of the oligonucleotide switches to the purine tract of the complementary strand of the duplex and is antiparallel to it. In contrast, with RNA as target, for a branched clamp oligonucleotide that formed a triple helix over its entire length (5'-TTCTTCAAAGGAGGG-3'.cxa.3'-GGGTGGTTT-T-GTTGTT-5') the portion of the Hoogsteen sequence that bound to the 3' extremity of the

target strand had to be antiparallel to it.
REFERENCE COUNT: 55 THERE ARE 55 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L31 ANSWER 17 OF 28 CA COPYRIGHT 2003 ACS
ACCESSION NUMBER: 133:145882 CA
TITLE: **Circular** DNA vectors for synthesis of RNA and DNA
INVENTOR(S): Kool, Eric T.
PATENT ASSIGNEE(S): University of Rochester, USA
SOURCE: U.S., 48 pp., Cont.-in-part of U.S. 5,714,320.
CODEN: USXXAM
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 6
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 6096880	A	20000801	US 1997-805631	19970226 <--
US 5714320	A	19980203	US 1995-393439	19950223 <--
US 6077668	A	20000620	US 1997-910632	19970813 <--
WO 9838300	A1	19980903	WO 1998-US3784	19980226 <--
W: JP				
RW: AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE				
EP 977839	A1	20000209	EP 1998-907649	19980226 <--
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, NL, SE, PT, IE, FI				
US 6368802	B1	20020409	US 2000-569344	20000511
US 2003087241	A1	20030508	US 2001-997931	20011130

PRIORITY APPLN. INFO.:
US 1993-47860 B2 19930415
US 1995-393439 A2 19950223
US 1997-805631 A2 19970226
WO 1998-US3784 W 19980226
US 2000-569344 A2 20000511

AB The present invention provides methods for synthesis, and therapeutic use of DNA and RNA oligonucleotides and analogs. RNA oligonucleotides are synthesized using a small, **circular** DNA template which lacks an RNA polymerase promoter sequence. The RNA synthesis is performed by combining a **circular** single-stranded oligonucleotide template with an effective RNA polymerase and at least two types of ribonucleotide triphosphate to form an RNA oligonucleotide multimer comprising multiple copies of the desired RNA oligonucleotide sequence. Preferably, the RNA oligonucleotide multimer is cleaved to produce RNA oligonucleotides having well-defined ends. Preferred RNA oligonucleotide multimers may contain ribozymes capable of both cis (autolytic) and trans cleavage, **antisense** RNA, or decoy RNA.
REFERENCE COUNT: 124 THERE ARE 124 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L31 ANSWER 18 OF 28 CA COPYRIGHT 2003 ACS
ACCESSION NUMBER: 130:48294 CA
TITLE: Efficient and simpler method to construct normalized cDNA libraries with improved representations of full-length cDNAs
INVENTOR(S): Soares, Marcelo Bento; Bonaldo, Mariade Fatima
PATENT ASSIGNEE(S): The Trustees of Columbia University In the City of New York, USA
SOURCE: U.S., 28 pp.
CODEN: USXXAM
DOCUMENT TYPE: Patent
LANGUAGE: English

FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 5846721	A	19981208	US 1996-715941	19960919 <--

PRIORITY APPLN. INFO.: US 1996-715941 19960919

AB This invention provides a method to normalize a cDNA library comprising: (a) constructing a directionally cloned library contg. cDNA inserts wherein the insert is capable of being amplified by polymerase chain reaction; (b) converting a double-stranded cDNA library into **single-stranded DNA circles**; (c) generating **single-stranded nucleic acid** mols. **complementary** to the **single-stranded DNA circles** converted in step (b) by polymerase chain reaction with appropriate primers; (d) hybridizing the **single-stranded DNA circles** converted in step (b) with the **complementary single-stranded nucleic acid** mols. generated in step (c) to produce partial duplexes to an appropriate C0t; and (e) sepg. the unhybridized **single-stranded DNA circles** from the hybridized DNA **circles**, thereby generating a normalized cDNA library. This invention also provides a method to normalize a cDNA library wherein the generating of **single-stranded nucleic acid** mols. **complementary** to the **single-stranded DNA circles** converted in step (b) is by excising cDNA inserts from the double-stranded cDNA library; purifying the cDNA inserts from cloning vectors; and digesting the cDNA inserts with an exonuclease. This invention further provides a method to construct a subtractive cDNA library following the steps described above. This invention further provides normalized and/or subtractive cDNA libraries generated by the above methods.

REFERENCE COUNT: 12 THERE ARE 12 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L31 ANSWER 19 OF 28 CA COPYRIGHT 2003 ACS
ACCESSION NUMBER: 129:226611 CA
TITLE: **Circular** DNA vectors for synthesis of RNA and DNA
INVENTOR(S): Kool, Eric T.
PATENT ASSIGNEE(S): University of Rochester, USA
SOURCE: PCT Int. Appl., 101 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 6
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9838300	A1	19980903	WO 1998-US3784	19980226 <--
W: JP				
RW: AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE				
US 6096880	A	20000801	US 1997-805631	19970226 <--
EP 977839	A1	20000209	EP 1998-907649	19980226 <--
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, NL, SE, PT, IE, FI				

PRIORITY APPLN. INFO.:
US 1997-805631 A 19970226
US 1993-47860 B2 19930415
US 1995-393439 A2 19950223
WO 1998-US3784 W 19980226

AB The present invention provides methods for synthesis and therapeutic use

of DNA and RNA oligonucleotides and analogs. RNA oligonucleotides are synthesized using a small, **circular** DNA template which lacks an RNA polymerase promoter sequence. The RNA synthesis is performed by combining a **circular** single-stranded oligonucleotide template with an effective RNA polymerase and at least two types of ribonucleotide triphosphate to form an RNA oligonucleotide multimer comprising multiple copies of the desired RNA oligonucleotide sequence. Preferably, the RNA oligonucleotide multimer is cleaved to produce RNA oligonucleotides having well-defined ends. Preferred RNA oligonucleotide multimers may contain ribozymes capable of both cis (autolytic) and trans cleavage, **antisense** RNA, or decoy RNA.

REFERENCE COUNT: 8 THERE ARE 8 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L31 ANSWER 20 OF 28 CA COPYRIGHT 2003 ACS
ACCESSION NUMBER: 128:98540 CA
TITLE: Procedure for normalization of cDNA libraries
INVENTOR(S): Bonaldo, Maria Defatima; Soares, Marcelo Bento
PATENT ASSIGNEE(S): Trustees of Columbia University In the City of New York, USA
SOURCE: U.S., 8 pp.
CODEN: USXXAM
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 5702898	A	19971230	US 1995-465857	19950606 <--

PRIORITY APPLN. INFO.: US 1995-465857 19950606

AB This invention provides a method to normalize a cDNA library constructed in a vector capable of being converted to single-stranded **circles** and capable of producing **complementary nucleic** acid mols. to the single-stranded **circles** comprising: (a) converting the cDNA library in single-stranded **circles**; (b) generating **complementary nucleic** acid mols. to the single-stranded **circles**; (c) hybridizing the single-stranded **circles** converted in step (a) with **complementary nucleic** acid mols. of step (b) to produce partial duplexes to an appropriate Cot; (e) sepg. the unhybridized single-stranded **circles** from the hybridized single-stranded **circles**, thereby generating a normalized cDNA library. The procedure has several advantages. First of all, because an excess of **complementary nucleic** acid mols. (**antisense** RNA) is used, there is no competition between full-length and truncated versions for complementary fragments and therefore there is no bias against longer clones. Second, since the synthesis is driven by an RNA promoter, even those clones without tail will be represented in the normalized library. Third, since the driver concn. is high, a Cot of 5-50 can be achieved in a few hours of incubation, thus making the procedure much quicker. Finally, only one step of hydroxylapatite purifn. is required, thus making the procedure considerably simpler and quicker. The procedure was applied to cDNA libraries from human placenta, breast tissue, pineal gland, retina, and ovarian tumor.

L31 ANSWER 21 OF 28 CA COPYRIGHT 2003 ACS
ACCESSION NUMBER: 124:309560 CA
TITLE: Target nucleic acid sequence amplification and detection using linear single-strand vector probe whose **circular** form transforms bacteria and method's forensic and clinical applications

INVENTOR(S): Marcolini, Stanislavo; Martinazzo, Giorgio
PATENT ASSIGNEE(S): Raggio-Italgene S.P.A., Italy
SOURCE: PCT Int. Appl., 29 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9603525	A1	19960208	WO 1995-EP2944	19950725 <--
W: AM, AT, AU, BB, BG, BR, BY, CA, CH, CN, CZ, DE, DK, EE, ES, FI, GB, GE, HU, IS, JP, KE, KG, KP, KR, KZ, LK, LR, LT, LU, LV, MD, MG, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, TJ, TM, TT				
RW: KE, MW, SD, SZ, UG, AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG				
AU 9533424	A1	19960222	AU 1995-33424	19950725 <--

PRIORITY APPLN. INFO.: GB 1994-14934 19940725
WO 1995-EP2944 19950725

AB A method for the detection of a target nucleic acid sequence in a sample, which comprises: (i) contacting the sample, which has been treated to bring any **nucleic acids** present into **single-stranded** form, (a) with a linear stranded vector-probe capable of transforming competent bacteria when in **circular** form, said vector-probe comprising a **nucleic** acid sequence **complementary** to the target nucleic acid sequence, and nucleic acid sequence being present in two parts, one part of said nucleic acid being present at the 5'-end of the vector-probe, the other part being present at the 3'-end, said vector-probe also comprising a region encoding a selectable or detectable marker, under conditions that permit hybridization of any target sequence present in the sample to the complementary sequence, and (b) with an enzyme capable or repairing a single-stranded break in a double-stranded nucleic acid structure; (ii) inactivating the repair enzyme; (iii) sepg. any resulting **circularized** single stranded linear vector-probe from the annealed target; (i.v.) contacting the **circularized** single stranded linear vector-probe, optionally in the form of the reaction mixt. resulting from step (ii), with competent host bacteria that lack the marker present in the vector-probe under transformation conditions; (v) culturing the resulting transformed bacteria and investigating the presence of the marker; and a vector for use in the method. The method may also be used for the detection and/or identification of mutations in a target nucleic acid sequence.

L31 ANSWER 22 OF 28 CA COPYRIGHT 2003 ACS
ACCESSION NUMBER: 122:126440 CA
TITLE: Solvent, pH, and ionic effects on the binding of **single-stranded DNA** by **circular** oligodeoxynucleotides
AUTHOR(S): D'Souza, David J.; Kool, Eric T.
CORPORATE SOURCE: Dep. Chem., Univ. Rochester, Rochester, NY, 14627, USA
SOURCE: Bioorganic & Medicinal Chemistry Letters (**1994**), 4(8), 965-70
CODEN: BMCLE8; ISSN: 0960-894X
DOCUMENT TYPE: Journal
LANGUAGE: English

AB The effects of changing soln. conditions on the strength of triple helical complexes formed between pyrimidine-rich **circular** DNA oligonucleotides and their homopurine complements are examd. The

complexes display properties different from those seen for other types of DNA triplexes.

L31 ANSWER 23 OF 28 CA COPYRIGHT 2003 ACS
ACCESSION NUMBER: 120:238465 CA
TITLE: Molecular recognition by **circular** oligonucleotides. Strong binding of **single-stranded DNA** and **RNA**. [Erratum to document cited in CA116(1):2426f]
AUTHOR(S): Prakash, Gautam; Kook, Eric T.
CORPORATE SOURCE: Dep. Chem., Univ. Rochester, Rochester, NY, 14627, USA
SOURCE: Journal of the Chemical Society, Chemical Communications (**1994**), (5), 676
CODEN: JCCCAT; ISSN: 0022-4936
DOCUMENT TYPE: Journal
LANGUAGE: English
AB The errors were not reflected in the abstr. or the index entries.

L31 ANSWER 24 OF 28 CA COPYRIGHT 2003 ACS
ACCESSION NUMBER: 116:2426 CA
TITLE: Molecular recognition by **circular** oligonucleotides. Strong binding of **single-stranded DNA** and **RNA**
AUTHOR(S): Prakash, Gautam; Kool, Eric T.
CORPORATE SOURCE: Dep. Chem., Univ. Rochester, Rochester, NY, 14627, USA
SOURCE: Journal of the Chemical Society, Chemical Communications (**1991**), (17), 1161-3
CODEN: JCCCAT; ISSN: 0022-4936
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Pyrimidine-rich **circular** DNA oligonucleotides display very high binding affinities for complementary RNA and DNA oligomers by forming bimol. triple-helical complexes.

L31 ANSWER 25 OF 28 SCISEARCH COPYRIGHT 2003 THOMSON ISI
ACCESSION NUMBER: 2000:27036 SCISEARCH
THE GENUINE ARTICLE: 269WH
TITLE: **Circular antisense** oligonucleotides inhibit growth of chronic myeloid leukemia cells
AUTHOR: Rowley P T (Reprint); Kosciolek B A; Kool E T
CORPORATE SOURCE: UNIV ROCHESTER, DIV GENET, BOX 641, ROCHESTER, NY 14642 (Reprint); UNIV ROCHESTER, DEPT MED, ROCHESTER, NY 14642; UNIV ROCHESTER, DEPT CHEM, ROCHESTER, NY 14642
COUNTRY OF AUTHOR: USA
SOURCE: MOLECULAR MEDICINE, (**OCT 1999**) Vol. 5, No. 10, pp. 693-700.
Publisher: SPRINGER VERLAG, 175 FIFTH AVE, NEW YORK, NY 10010.
ISSN: 1076-1551.
DOCUMENT TYPE: Article; Journal
FILE SEGMENT: LIFE; CLIN
LANGUAGE: English
REFERENCE COUNT: 32
ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS
AB Background: **Antisense** represents a conceptually powerful method for regulating gene expression. However, **antisense** oligonucleotides developed to date manifest two serious limitations-nuclease susceptibility and nonspecific hybridization. **Circular** oligonucleotides may be superior to conventional linear oligonucleotides in both respects. First, **circular** agents, having no ends, are exonuclease-resistant. Second, they bind to complementary strands of RNA and DNA with a higher affinity than

corresponding linear agents.

Methods and Results: We assessed the activity of **circular** phosphodiester deoxynucleotides using chronic myeloid cell lines by targeting polypurine sequences. To represent cells having a bcr3/abl2-type junction, we used K562 cells. A **circle** targeting a bcr polypurine sequence 385 nucleotides 5' to the junction decreased the cell number by day 5 with an IC50 of 9 mu M. To represent cells having a bcr2/abl2-type junction, we used BV173 cells. A **circle** targeting the bcr-abl junction itself decreased the cell number by day 7 with an IC50 of 8 mu M. Control oligonucleotides, whether the same sequence uncircularized or **circles** with the same nucleotide composition but in scrambled sequence, had little effect. Unlike linear agents, **circles** were stable when incubated in 10% serum. The amount of ba-abl protein detected by Western blotting using a specific anti-ba-abl antibody at 24 hr in **antisense**-treated BV173 cells was only 10% of that of cells treated with control **circles**, which demonstrates an **antisense** mechanism of action.

Conclusions: **Circular** oligodeoxyribonucleotides (1) inhibit the accumulation of CML cells, (2) decrease the amount of bcr-abl protein per cell, (3) have sequence-selective activity, and (4) are more active than linear oligonucleotides containing only the base-pairing region.

L31 ANSWER 26 OF 28 SCISEARCH COPYRIGHT 2003 THOMSON ISI
ACCESSION NUMBER: 1998:466314 SCISEARCH
THE GENUINE ARTICLE: ZT689
TITLE: Replication and control of **circular** bacterial plasmids
AUTHOR: delSolar G; Giraldo R; RuizEchevarria M J; Espinosa M; DiazOrejas R (Reprint)
CORPORATE SOURCE: CSIC, CTR INVEST BIOL, VELAZQUEZ 144, E-28006 MADRID, SPAIN (Reprint); CSIC, CTR INVEST BIOL, E-28006 MADRID, SPAIN
COUNTRY OF AUTHOR: SPAIN
SOURCE: MICROBIOLOGY AND MOLECULAR BIOLOGY REVIEWS, (**JUN 1998**) Vol. 62, No. 2, pp. 434-&.
Publisher: AMER SOC MICROBIOLOGY, 1325 MASSACHUSETTS AVENUE, NW, WASHINGTON, DC 20005-4171.
ISSN: 1092-2172.
DOCUMENT TYPE: General Review; Journal
FILE SEGMENT: LIFE
LANGUAGE: English
REFERENCE COUNT: 350

ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

AB An essential feature of bacterial plasmids is their ability to replicate as autonomous genetic elements in a controlled way within the host. Therefore, they can be used to explore the mechanisms involved in DNA replication and to analyze the different strategies that couple DNA replication to other critical events in the cell cycle. In this review, we focus on replication and its control in **circular** plasmids. Plasmid replication can be conveniently divided into three stages: initiation, elongation, and termination. The inability of DNA polymerases to initiate de novo replication makes necessary the independent generation of a primer. This is solved in **circular** plasmids, by two main strategies: (i) opening of the strands followed by RNA priming (theta and strand displacement replication) or (ii) cleavage of one of the DNA strands to generate a 3'-OH end (rolling-**circle** replication). Initiation is catalyzed most frequently by one or a few plasmid-encoded initiation proteins that recognize plasmid-specific DNA sequences and determine the point from which replication starts (the origin of replication). In some cases, these proteins also participate directly in the generation of the primer. These initiators can also play the role of pilot proteins that guide the assembly of the host replisome at the

plasmid origin. Elongation of plasmid replication is carried out basically by DNA polymerase III holoenzyme land, in some cases, by DNA polymerase I at an early stage), with the participation of other host proteins that form the replisome. Termination of replication has specific requirements and implications for reinitiation, studies of which have started. The initiation stage plays an additional tale: it is the stage at which mechanisms controlling replication operate. The objective of this control is to maintain a fixed concentration of plasmid molecules in a growing bacterial population (duplication of the plasmid pool paced with duplication of the bacterial population). The molecules involved directly in this control can be (i) RNA (**antisense** RNA), (ii) DNA sequences (iterons), or (iii) **antisense** RNA and proteins acting in concert. The control elements maintain an average frequency of one plasmid replication per plasmid copy per cell cycle and can ''sense'' and correct deviations from this average. Most of the current knowledge on plasmid replication and its control is based on the results of analyses performed with pure cultures under steady-state growth conditions. This knowledge sets important parameters needed to understand the maintenance of these genetic elements in mixed populations and under environmental conditions.

L31 ANSWER 27 OF 28 SCISEARCH COPYRIGHT 2003 THOMSON ISI
ACCESSION NUMBER: 95:406575 SCISEARCH
THE GENUINE ARTICLE: RB956
TITLE: SYNTHESIS OF **CIRCULAR** OLIGODEOXYNUCLEOTIDE CONJUGATES VIA TRANSIENT ABASIC SITES
AUTHOR: PEOCH D; IMBACH J L; RAYNER B (Reprint)
CORPORATE SOURCE: UNIV MONTPELLIER 2, CHIM BIOORGAN LAB, CNRS, URA 488, CASE 008, PL EUGENE BATAILLON, F-34095 MONTPELLIER, FRANCE (Reprint); UNIV MONTPELLIER 2, CHIM BIOORGAN LAB, CNRS, URA 488, F-34095 MONTPELLIER, FRANCE
COUNTRY OF AUTHOR: FRANCE
SOURCE: NUCLEOSIDES AND NUCLEOTIDES, (**1995**) Vol. 14, No. 3-5, pp. 847-850.
ISSN: 0732-8311.
DOCUMENT TYPE: Article; Journal
FILE SEGMENT: LIFE
LANGUAGE: ENGLISH
REFERENCE COUNT: 7
ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

AB New chemical ligation or cyclisation reactions, using high reactivity of abasic sites with amines, are reported for the synthesis of oligonucleotide clamps and single-stranded **circular** oligonucleotides. Thermal denaturation experiments show that these molecules display very high binding affinities for **complementary** DNA **oligomer** by forming triple-helical complexes.

L31 ANSWER 28 OF 28 SCISEARCH COPYRIGHT 2003 THOMSON ISI
ACCESSION NUMBER: 95:131940 SCISEARCH
THE GENUINE ARTICLE: QG046
TITLE: HISTONES ASSOCIATED WITH **SINGLE-STRANDED -DNA** DO NOT PRECLUDE THE FORMATION OF DOUBLE-HELICAL DNA
AUTHOR: FERNANDEZBUSQUETS X; DABAN J R (Reprint)
CORPORATE SOURCE: UNIV AUTONOMA BARCELONA, FAC CIENCIES, DEPT BIOQUIM & BIOL MOLEC, E-08193 BARCELONA, SPAIN (Reprint); UNIV AUTONOMA BARCELONA, FAC CIENCIES, DEPT BIOQUIM & BIOL MOLEC, E-08193 BARCELONA, SPAIN
COUNTRY OF AUTHOR: SPAIN
SOURCE: BIOCHIMICA ET BIOPHYSICA ACTA-GENE STRUCTURE AND EXPRESSION, (**25 JAN 1995**) Vol. 1260, No. 2, pp. 132-138.

ISSN: 0167-4781.
DOCUMENT TYPE: Article; Journal
FILE SEGMENT: LIFE
LANGUAGE: ENGLISH
REFERENCE COUNT: 26
ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

AB The effect of histones on the reaction of reassociation of the two complementary strands of DNA from different sources has been investigated. The reassociation rate of denatured linear DNA from bacteriophage M13 monitored spectrophotometrically and using nuclease S1 is roughly the same in the presence and absence of core histones at physiological ionic strength. Electron microscopy reveals that in the samples containing histones a large network of duplex DNA is produced. Nevertheless, closed **circular** M13 DNA and a cloned DNA fragment (158 bp) from nucleosomal origin are entirely renatured in the presence of histones as demonstrated by the well-defined double-stranded DNA bands seen in electrophoretic gels. Various experiments performed using the purified (+) and (-) strands of the cloned nucleosome DNA fragment at low ionic strength indicate that core histones initially bound to one or even to the two strands allow the formation of duplex DNA. These findings and the results obtained with partially denatured closed **circular** M13 DNA allow us to conclude that core histones neither prevent the nucleation nor inhibit the rapid zippering reactions leading to the formation of double-stranded DNA. The mechanism that allows the renaturation of DNA in the presence of histones may also participate in biological processes involving the pairing of **complementary nucleotides**.